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FIGURE 1

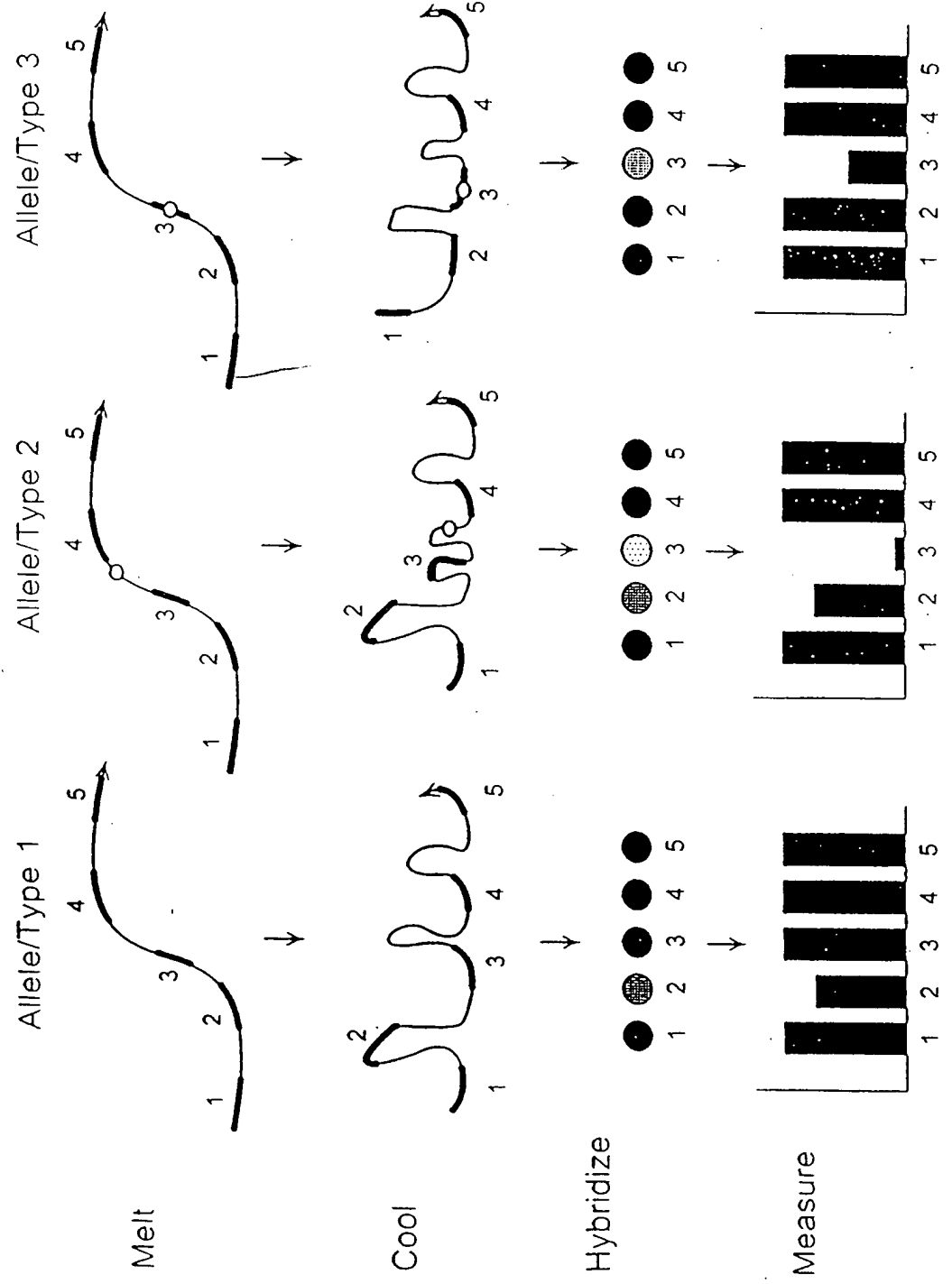


FIGURE 2

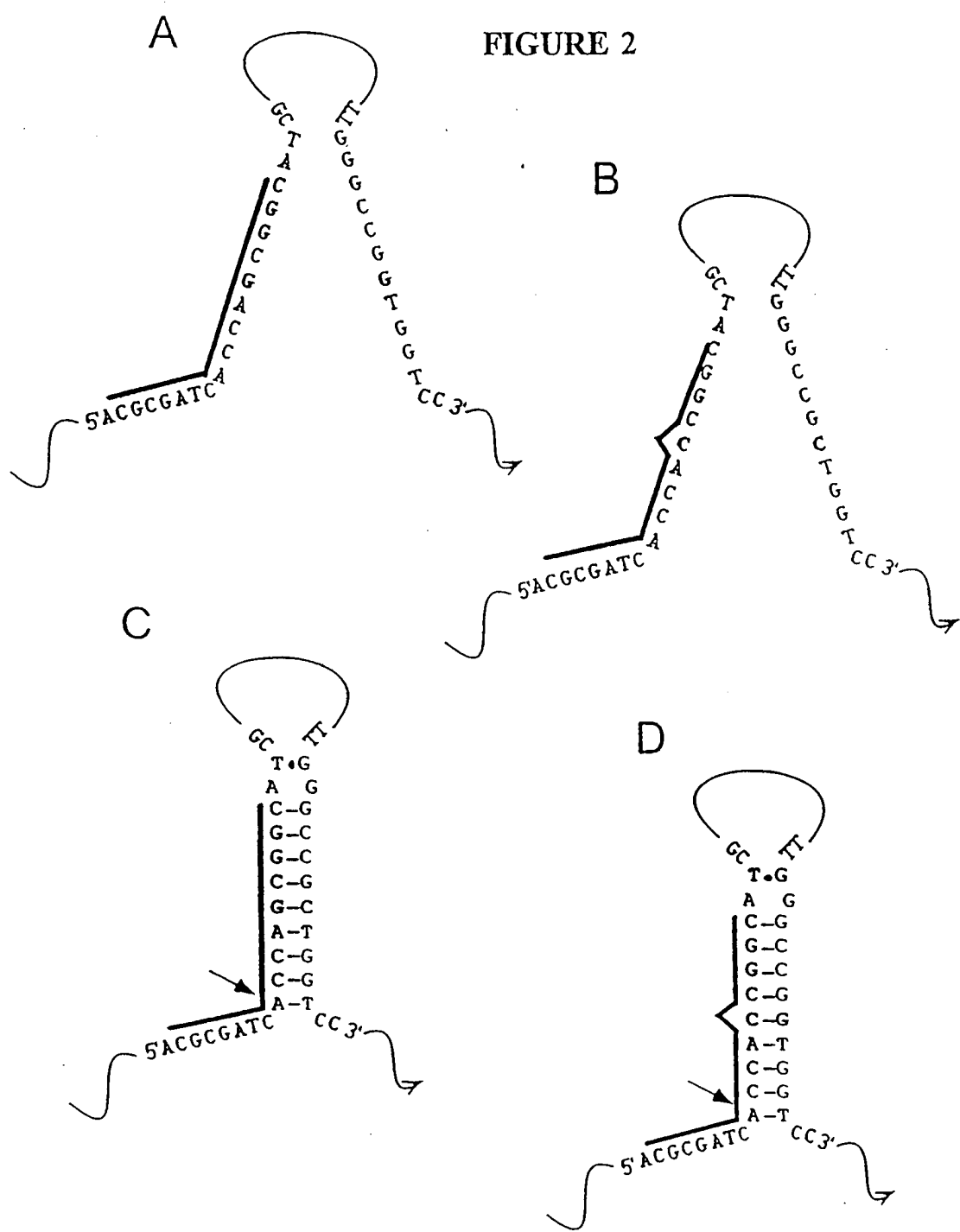


FIGURE 3

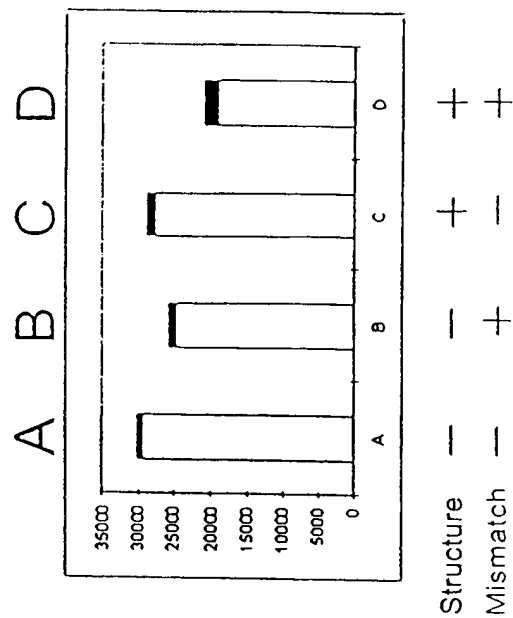
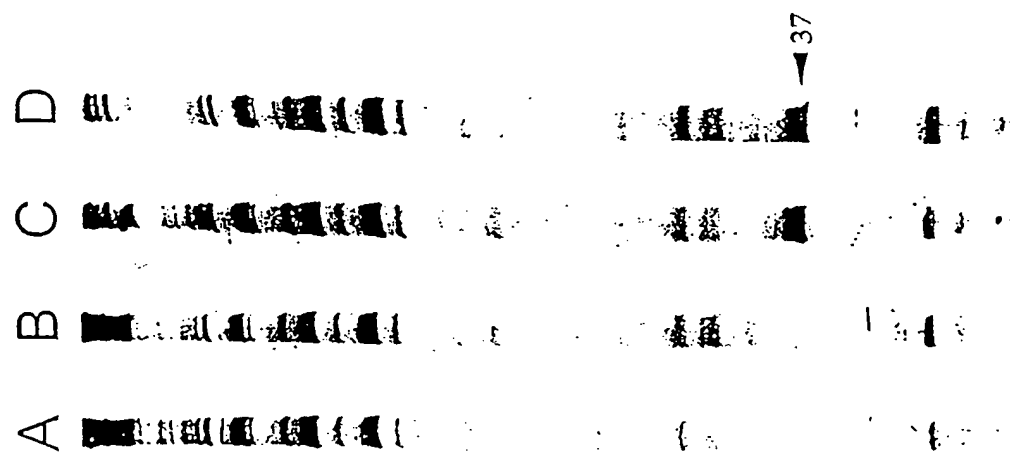


FIGURE 4

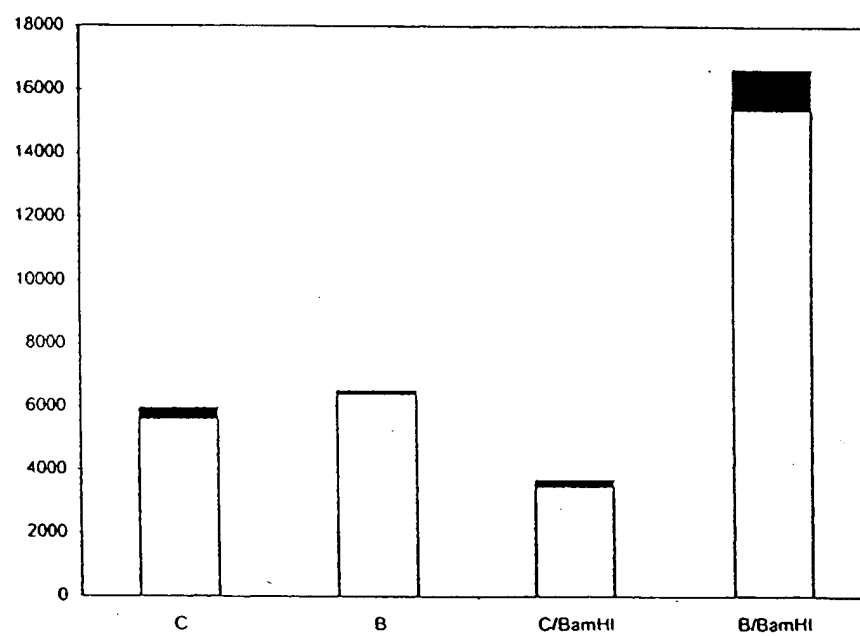


FIGURE 5

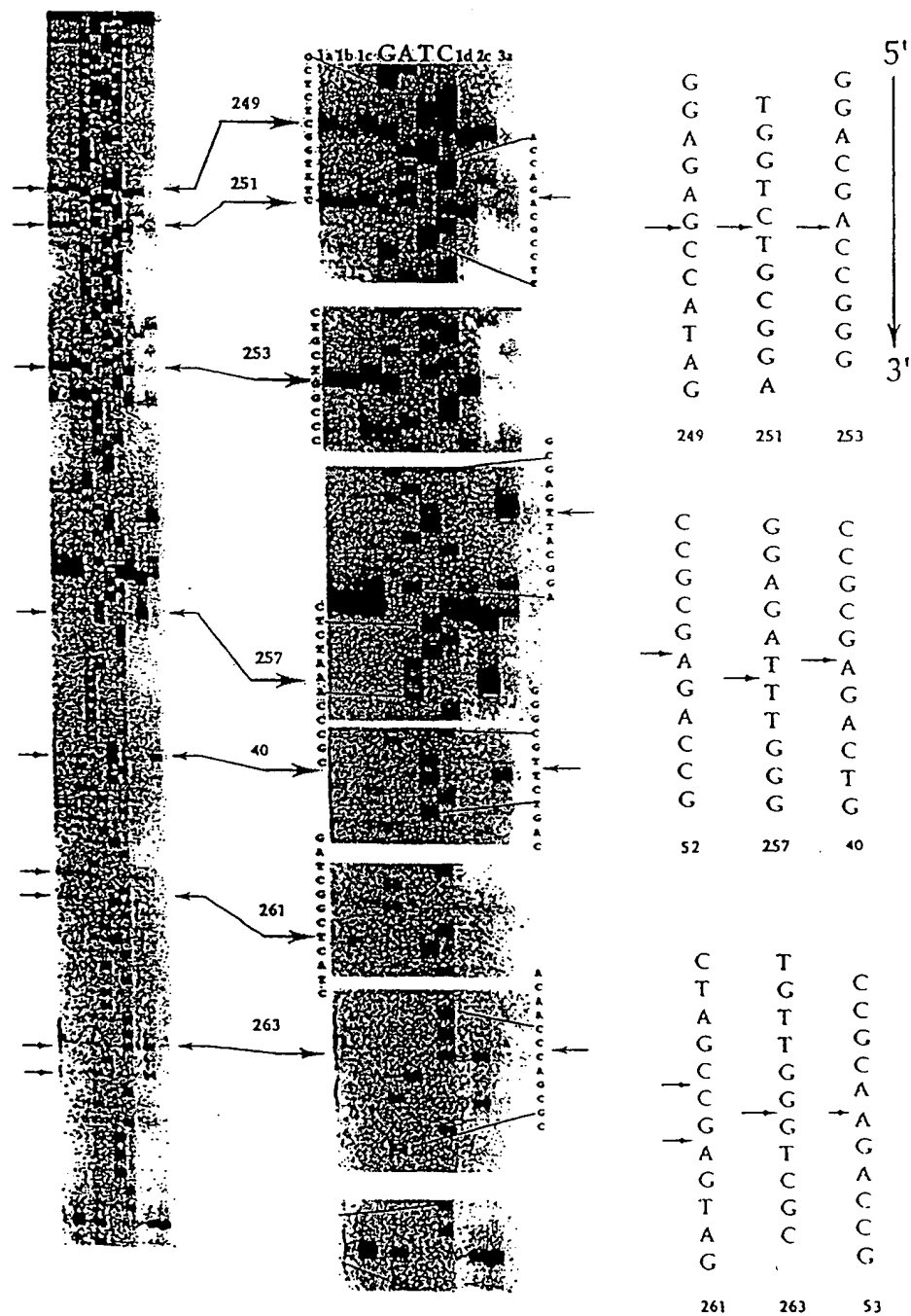


FIGURE 6

Consensus:	GATTCTGTCT	TCACGCAGAA	AGCGTCTAGC	CATGGCGTTA	GTATGAGTGT	CGTGACGCCT
HCV 1a	-----	-----	-----	-----	-----	-----
HCV 1b	-----	-----	-----	-----	-----	-----
HCV 2c	-----	-----	-----	-----	-----	-A-----
HCV 3a	-----	-----	-C-----	-----	-C-----	-----

	#249	#251
CCAGGACCCC	<u>CCCTCCCCGGG AGAGCCATAG</u>	<u>TGGTCTGCGG AACCGGTGAG</u> TACACCGGAA
-----	-----	-----
-T-----	-----	-----
-C-----	-----	-----
-----	-A-----	-----

	#253	#257
TTGCCAGGAC	<u>GACCGGGTCC</u> TTTCTTGGAT	CAACCCGCTC <u>AATGCCCTGGA</u> GATTGGGCG
-----	-----	-----
-----	-----	-----
-G--A	-T-----	A--A--T--C-C C--
-C-TG-GT	-----	-G-----A-CA- A--

	#40	#261	#263
TGCCCCCGCA	<u>AGACTGCTAG</u> CCGAGTAGTG	<u>TTGGGTGCGG</u> AAAGGCCTTG	TGGTACTGCC
-----	-----	-----	-----
-G-----	-----	-----	-----
-----	-----	-C-----T--	-----
-G-----	-TCA-----	-----	-----

TGATAGGGTG	CTTGCGAGTG	CCCCGGGAGG	TCTCGTAGAC	CGTGCAATC
-----	-----	-----	-----	-----
-----	-----	-----	-----	-----
-----	-A-----	-----	-----	-----
-----	-----	-----	-----	-----

FIGURE 7

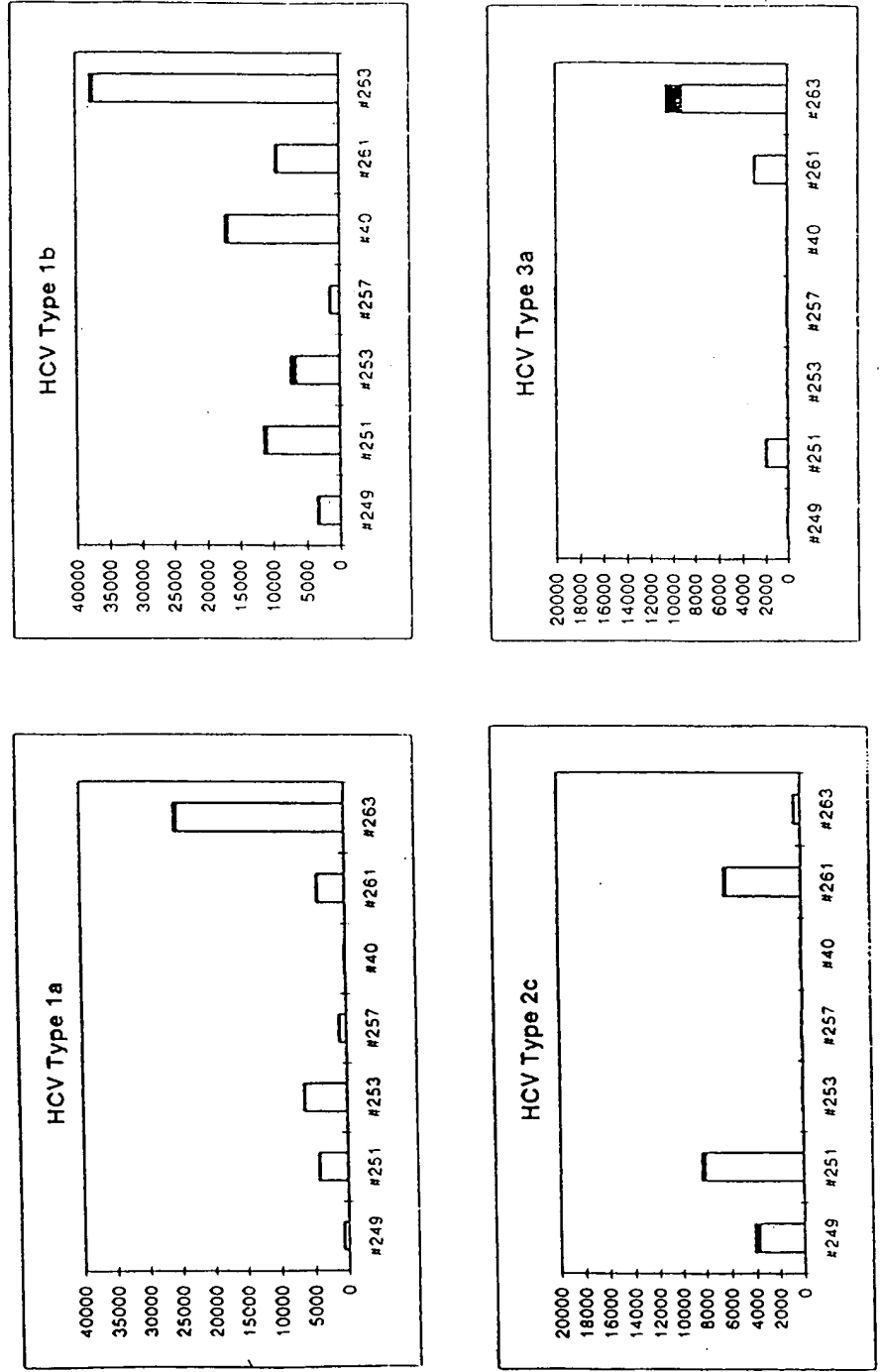


FIGURE 8A

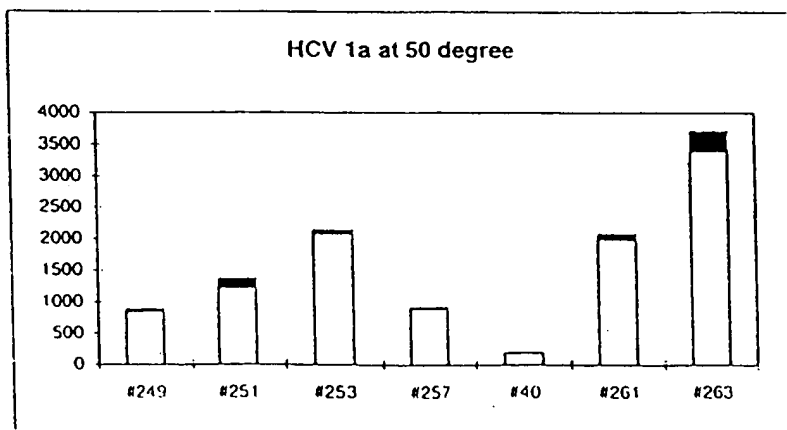
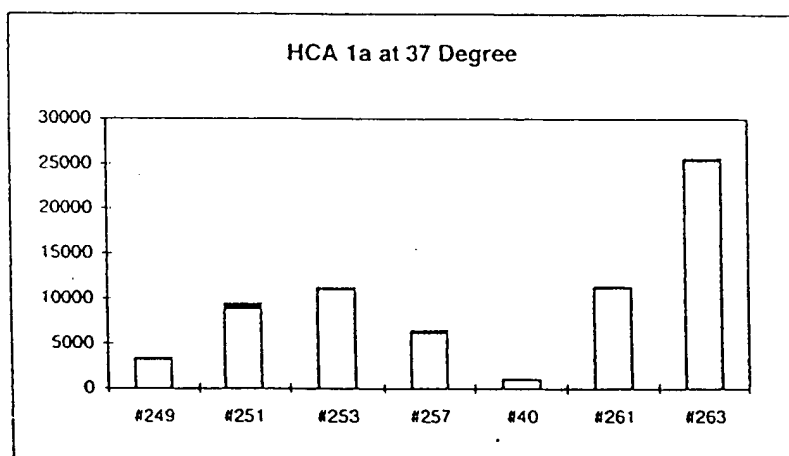
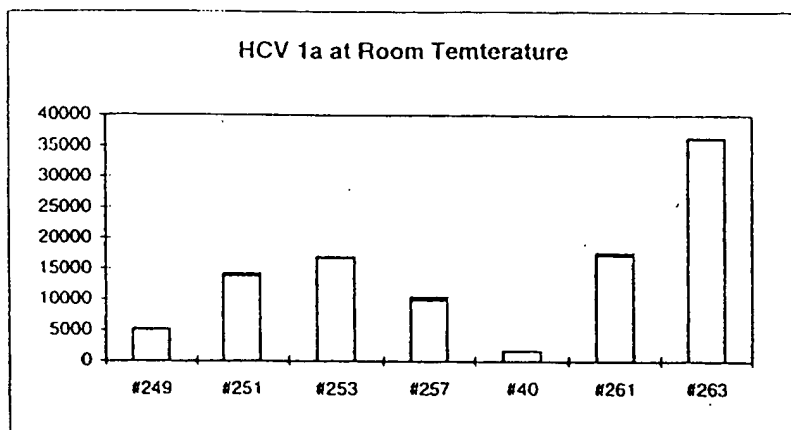


FIGURE 8B

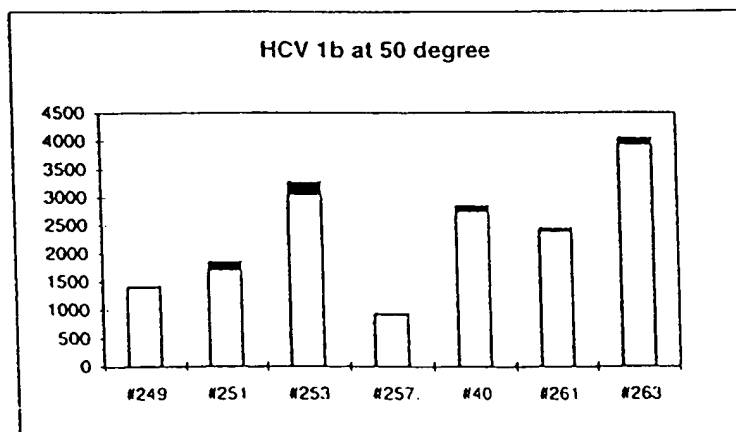
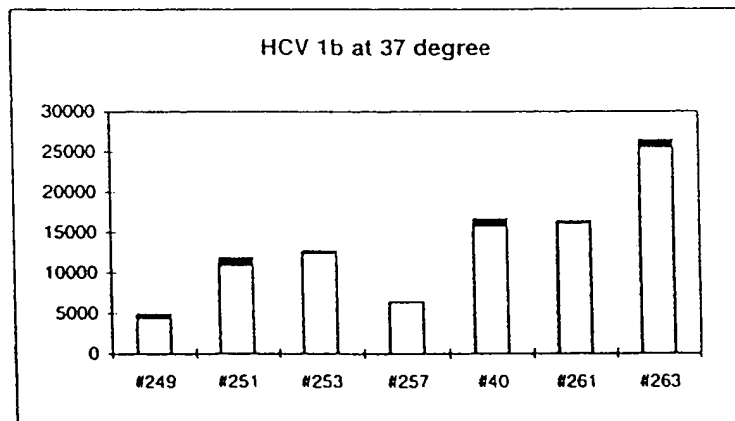
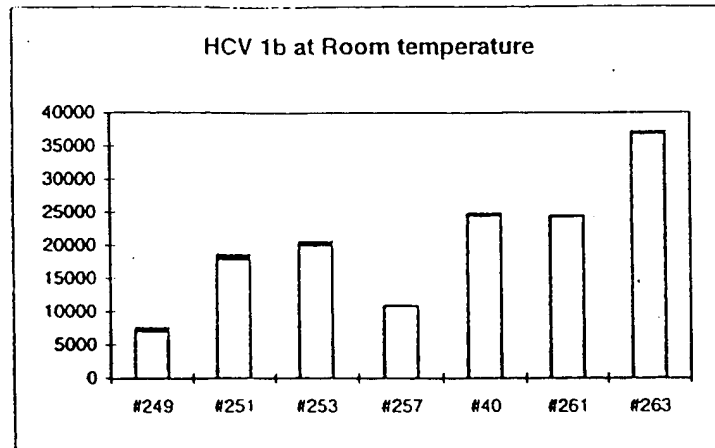


FIGURE 8C

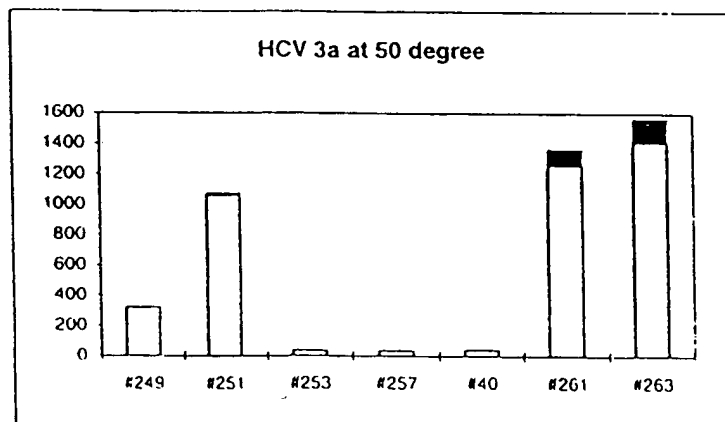
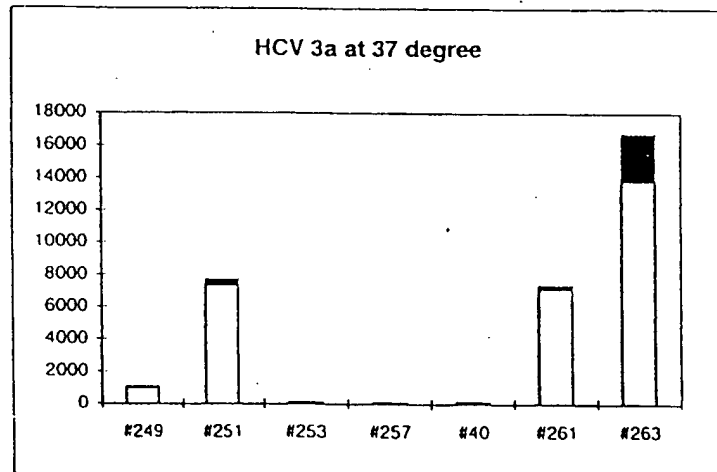
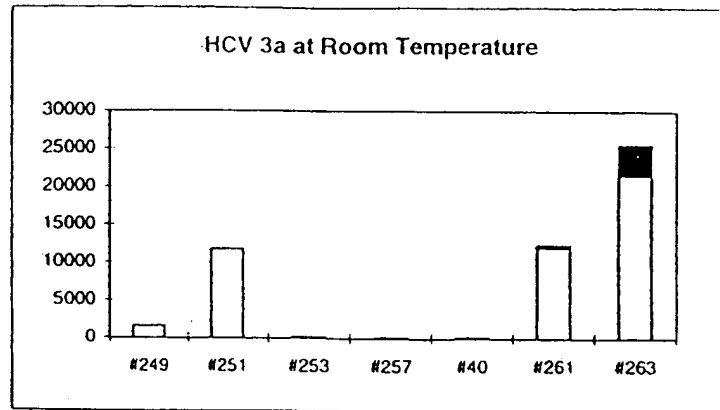


FIGURE 9A

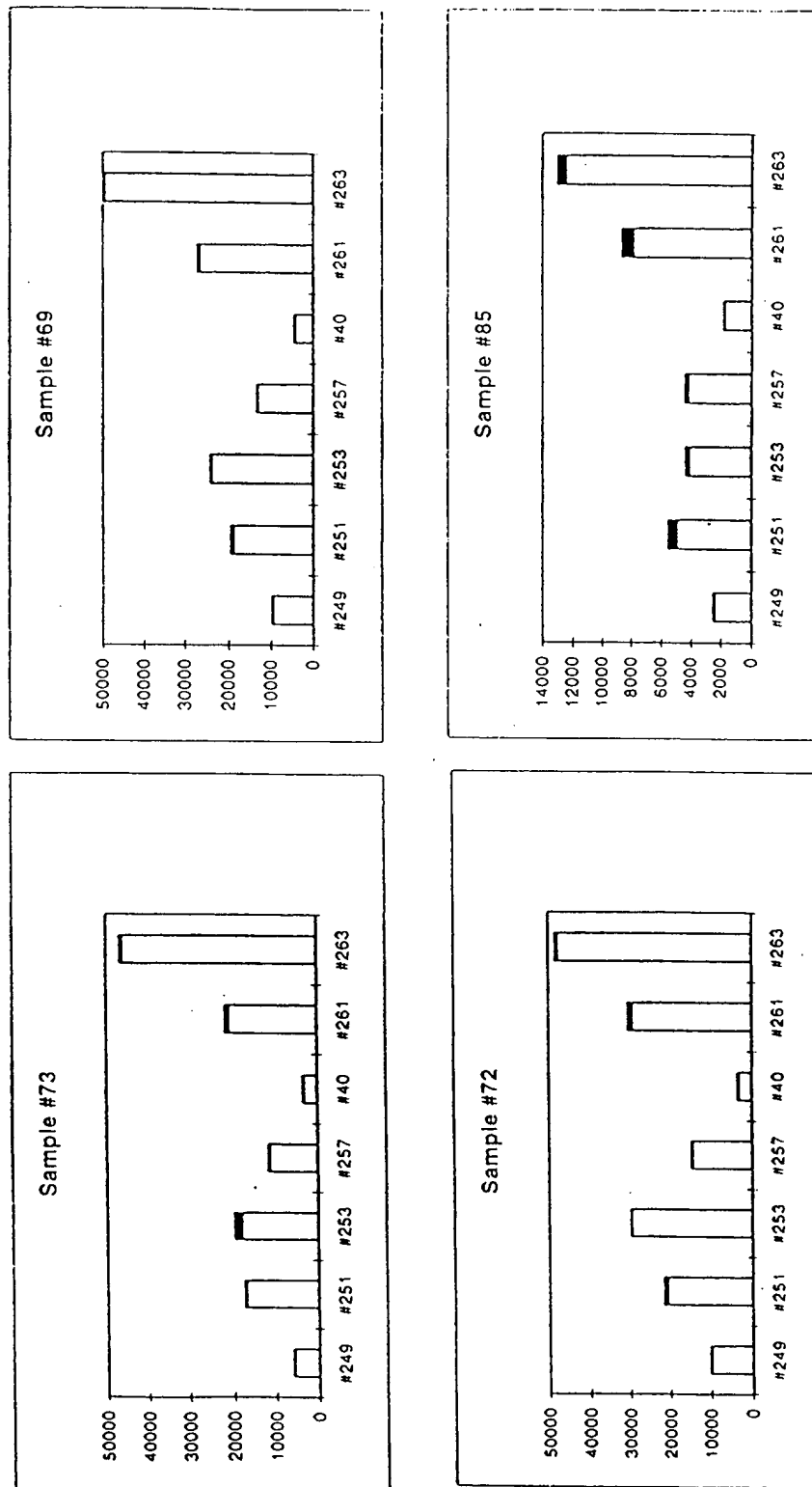


FIGURE 9B

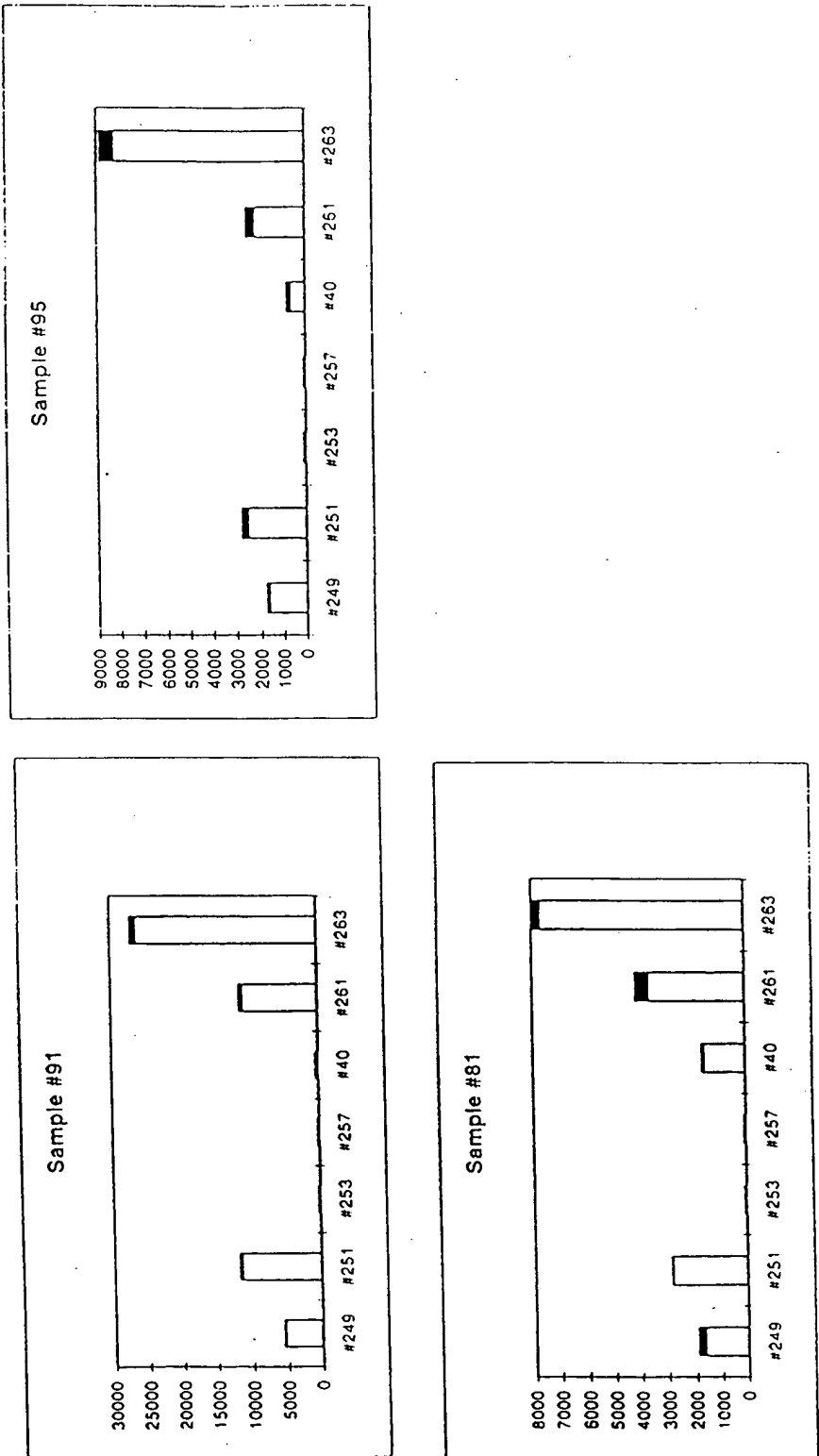


FIGURE 9C

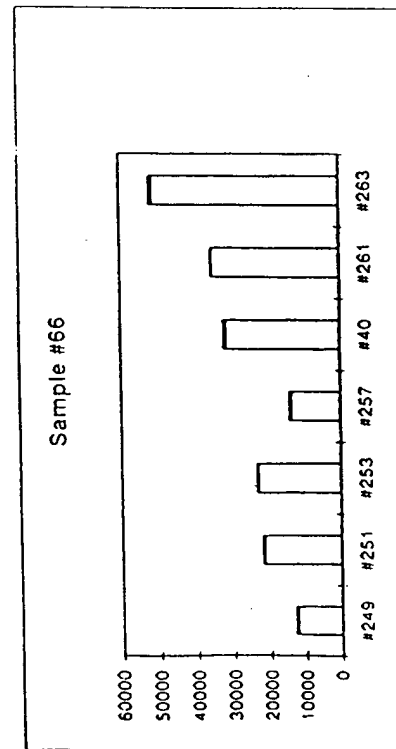
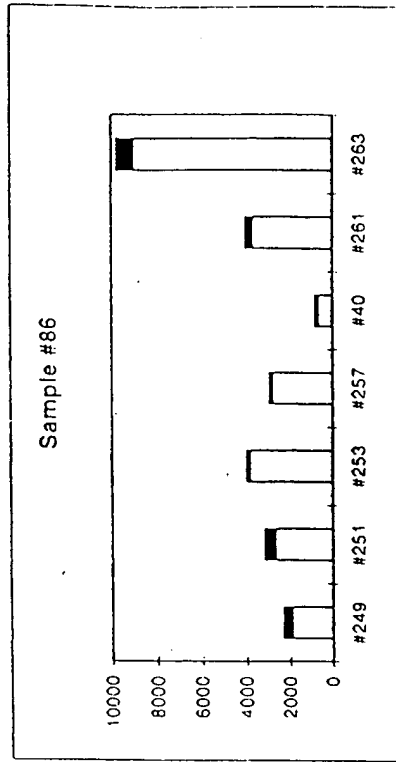


FIGURE 9D

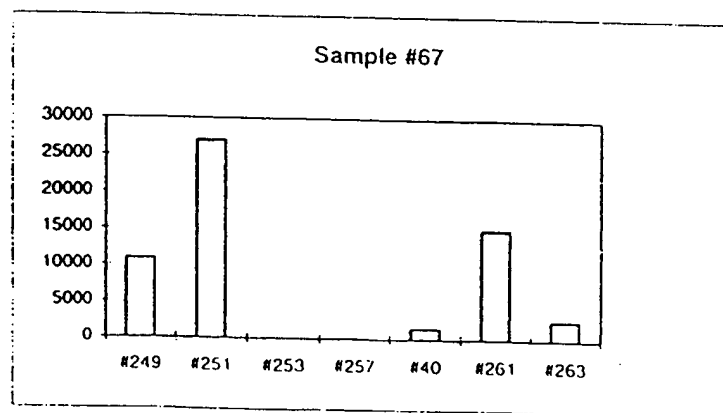
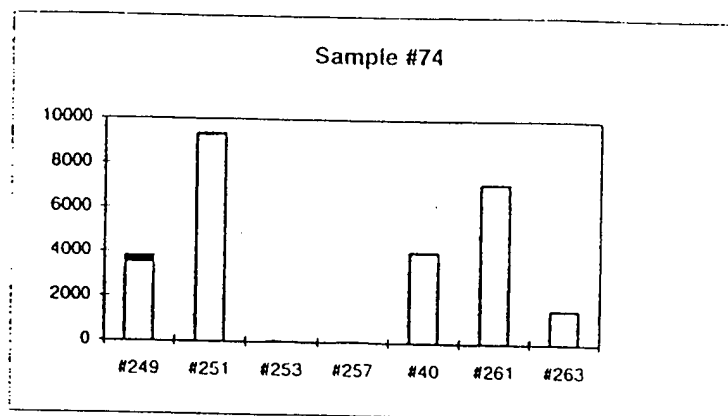


FIGURE 10

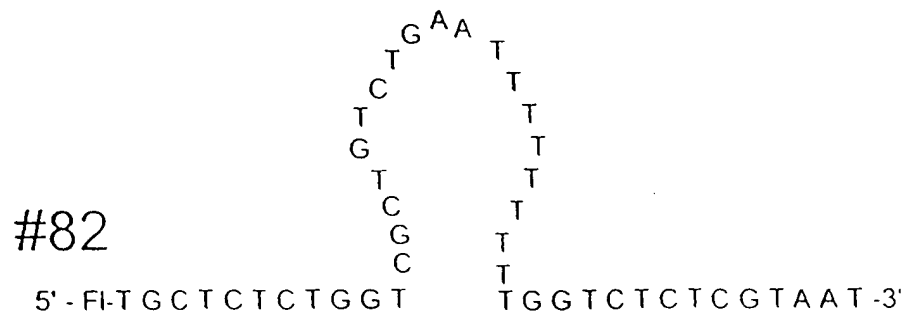
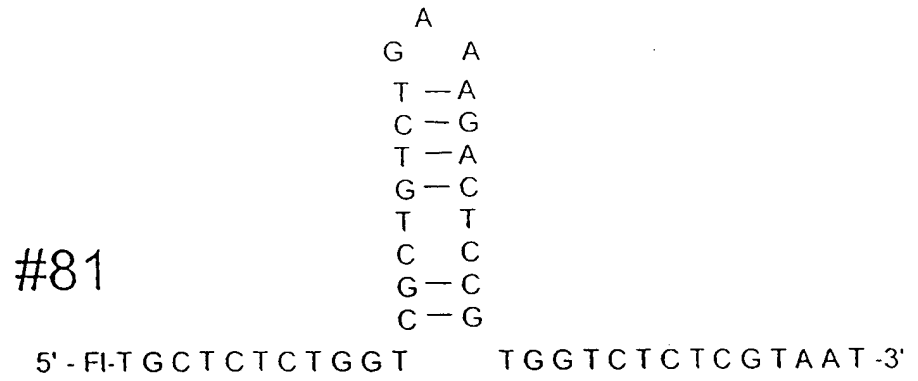
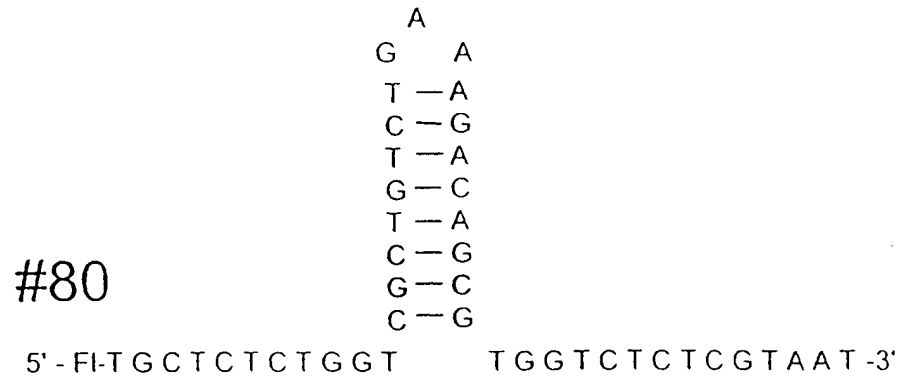


FIGURE 11A

#2) 5' Biotin

```

      I
      T   A
    C   G   A
    A   T - A
    G   C - G
    A   T - A
    C   G - C
    A   T - A
    G   C - G
    C   G - C
    G   C - G
  
```

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#91) 3' Biotin - CGAGAGACCA-5'

```

      A
    G   A
    T - A
    C - G
    T - A
    G - C
    T - A
    C - G
    G - C
    C - G
  
```

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#78) 3' - AGACCATTACCAGA -Biotin 5'

#4) 3' - GAGACCATTACCAGAG -Biotin 5'

#79) 3' - AGAGACCATTACCAGAGA -Biotin 5'

↓ ↓

#116) 3' - AGAGACCAACCAGAGA -Biotin 5'

#117) 3' - TACCAGAGA -Biotin 5'

#118) 3' - AGAGACCAT - 5'

FIGURE 11B

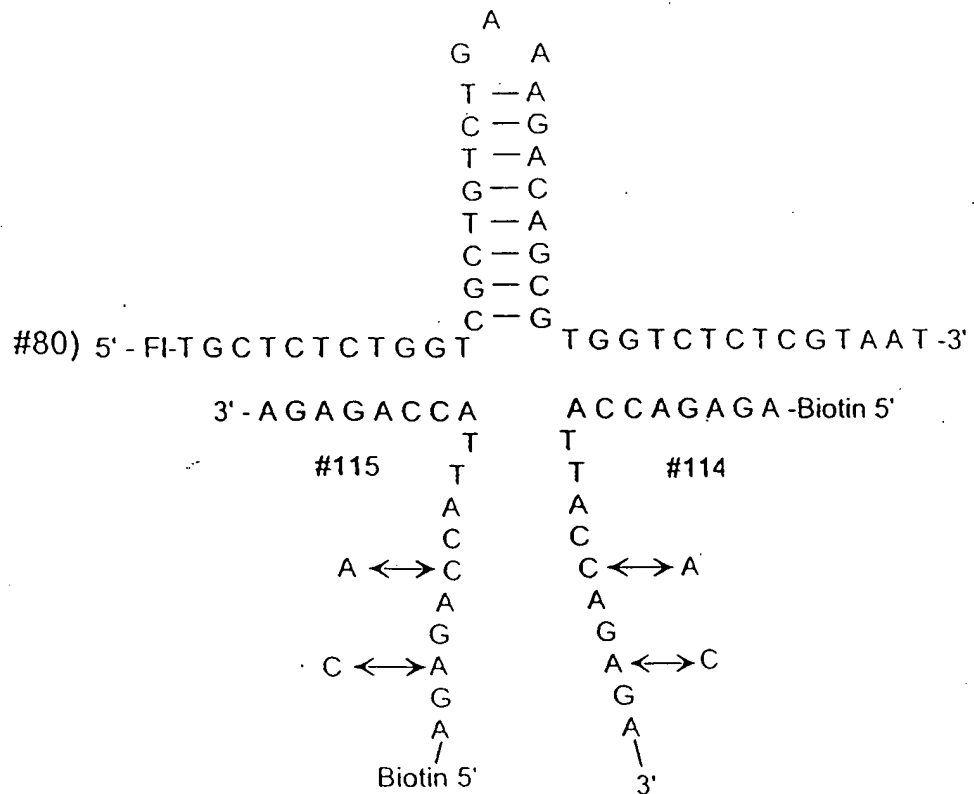
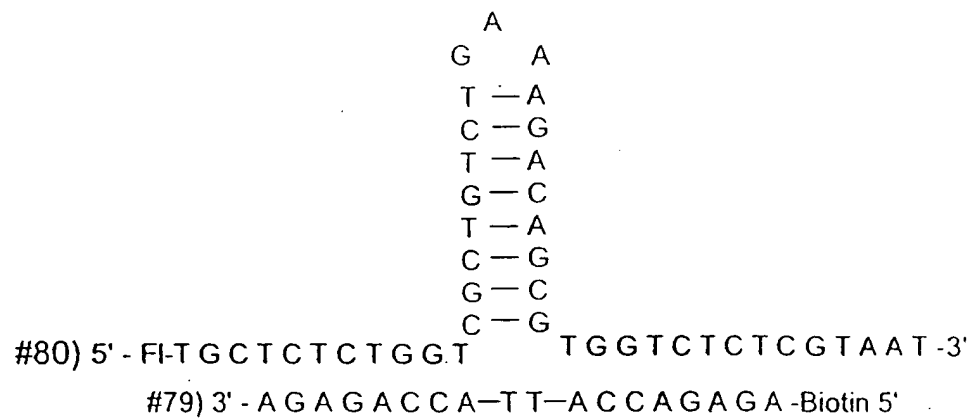
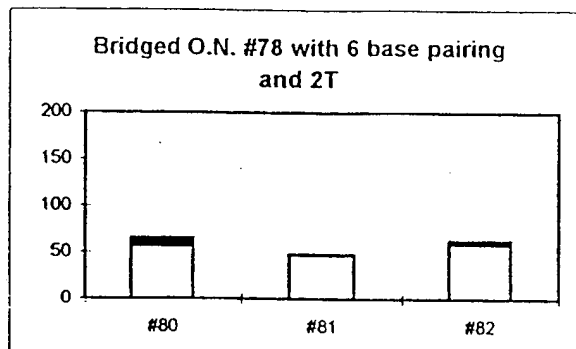
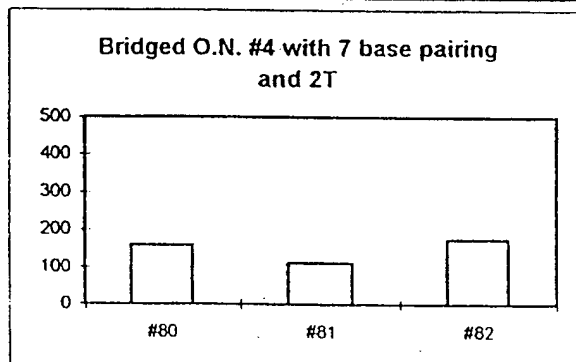


FIGURE 12

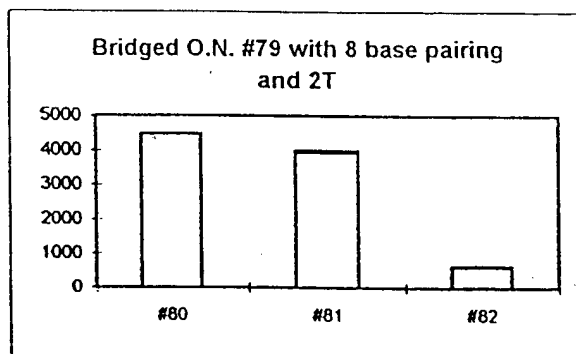
A



B



C



D

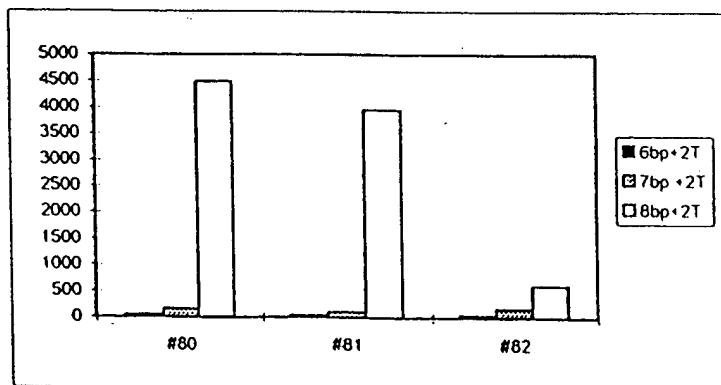


FIGURE 13A

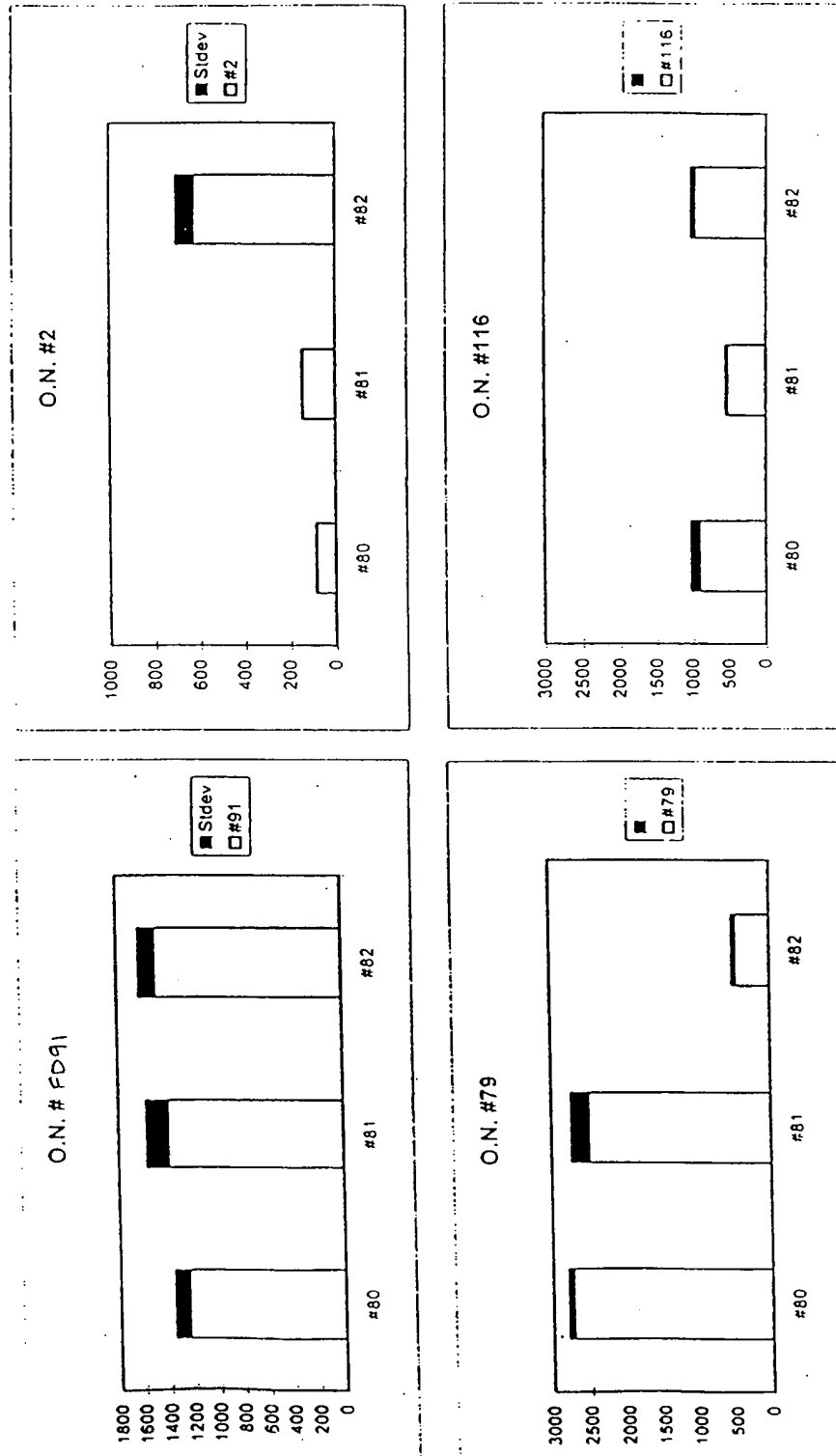


FIGURE 13B

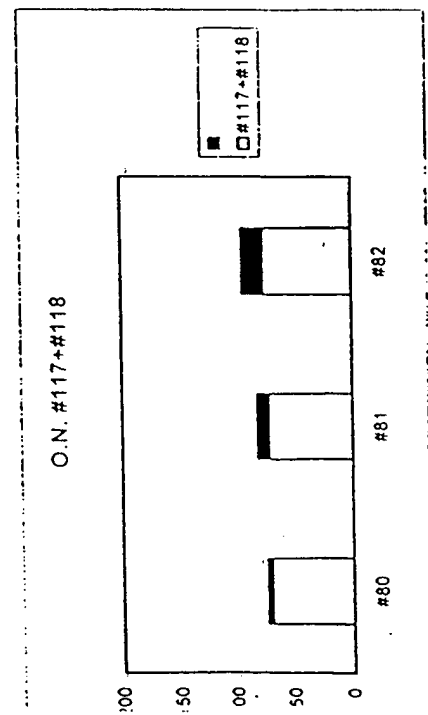
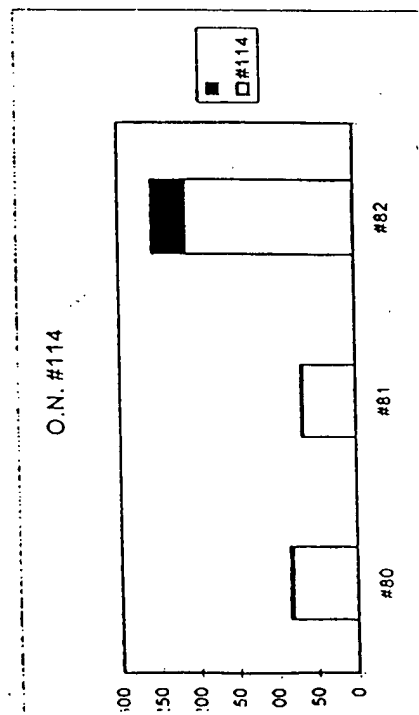
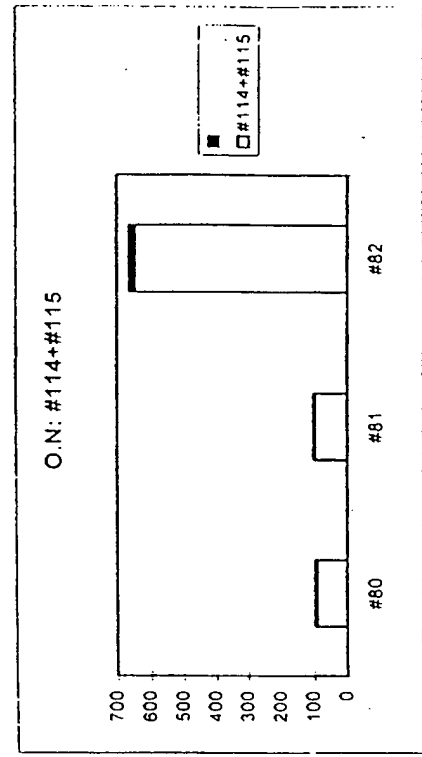
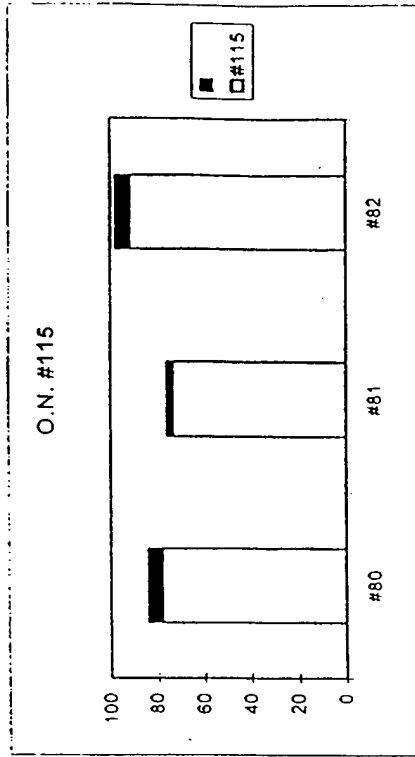


FIGURE 14

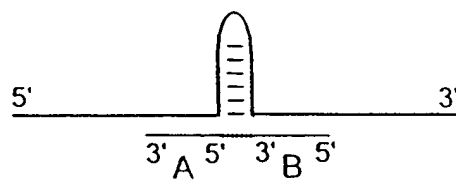
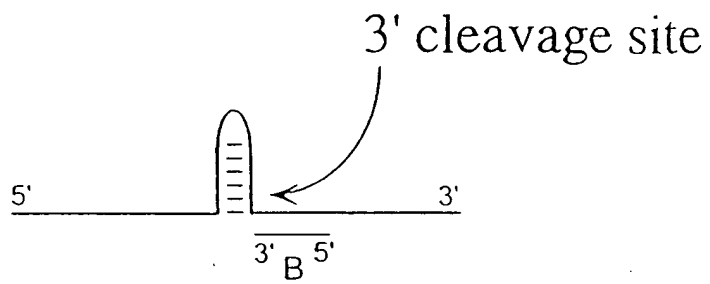
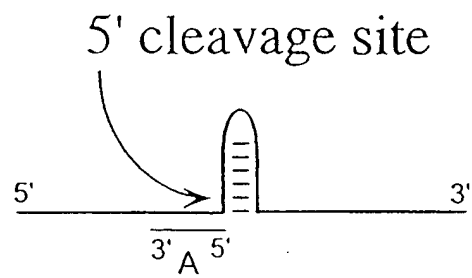


FIGURE 15

[illegible]

FIGURE 16A

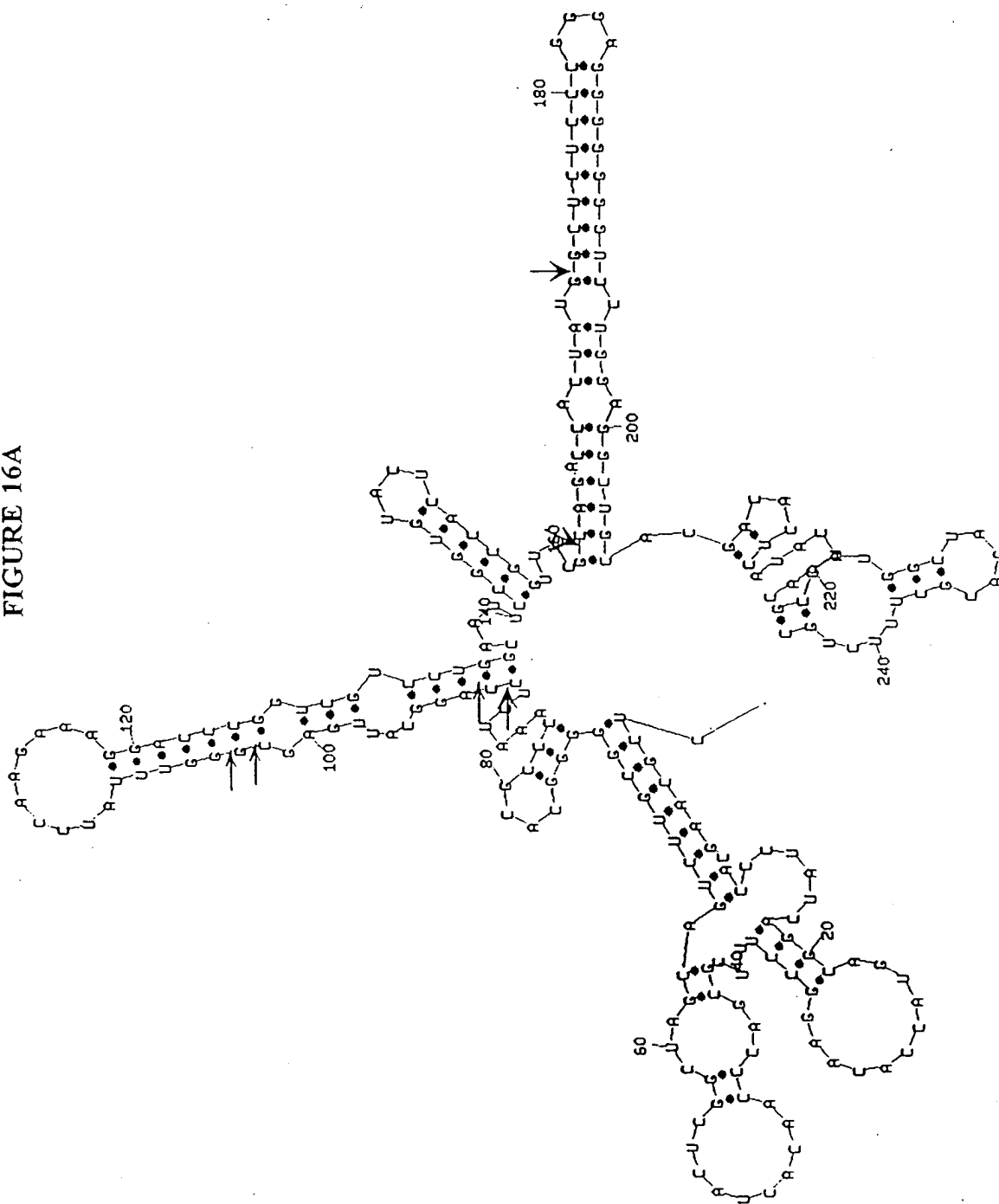


FIGURE 16B

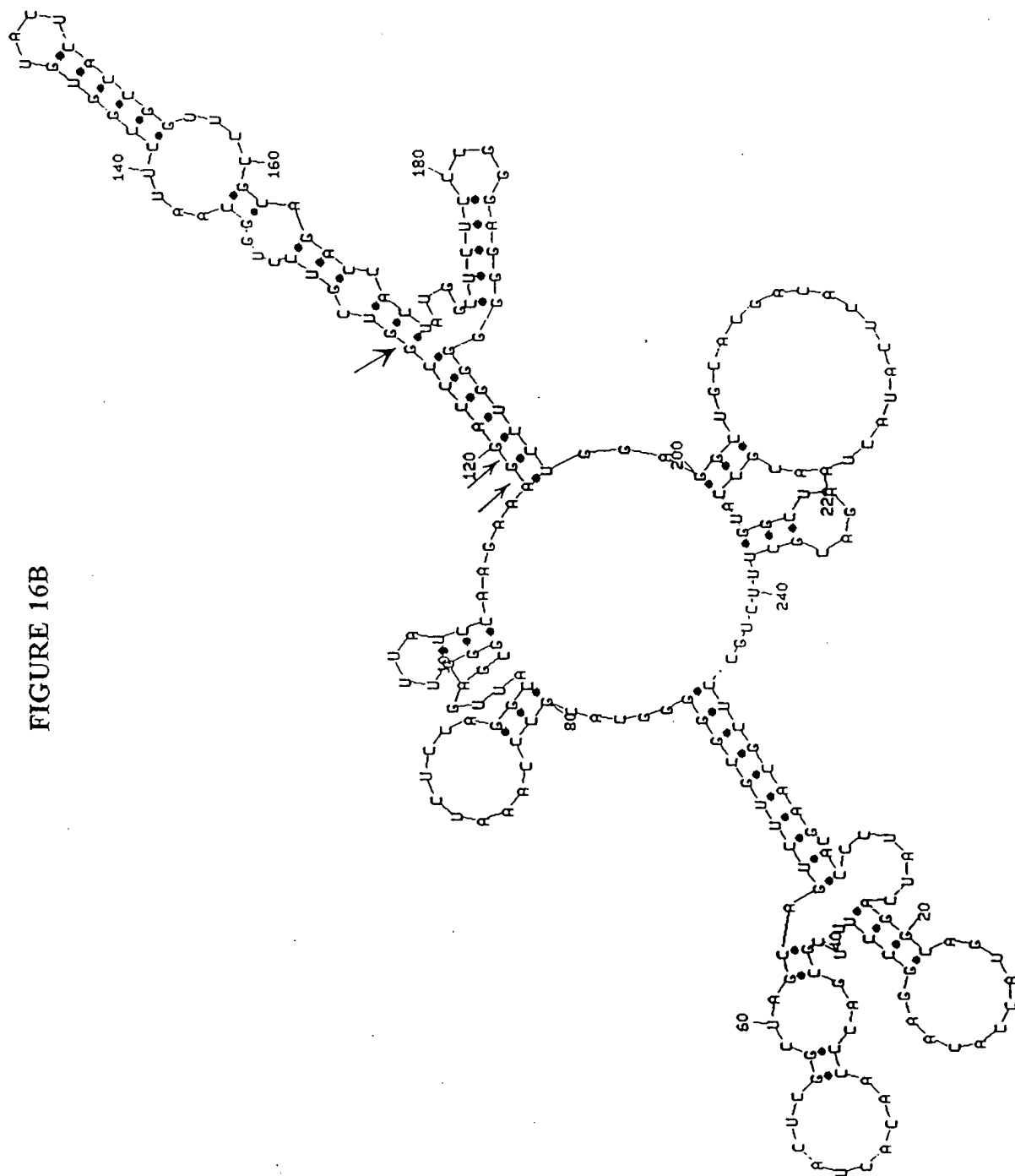


FIGURE 17A

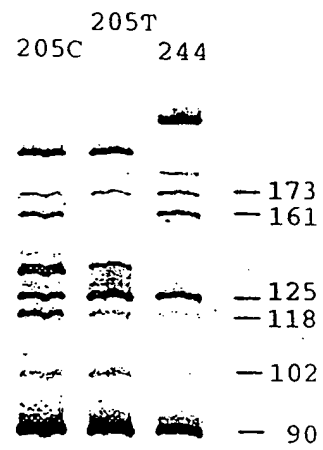
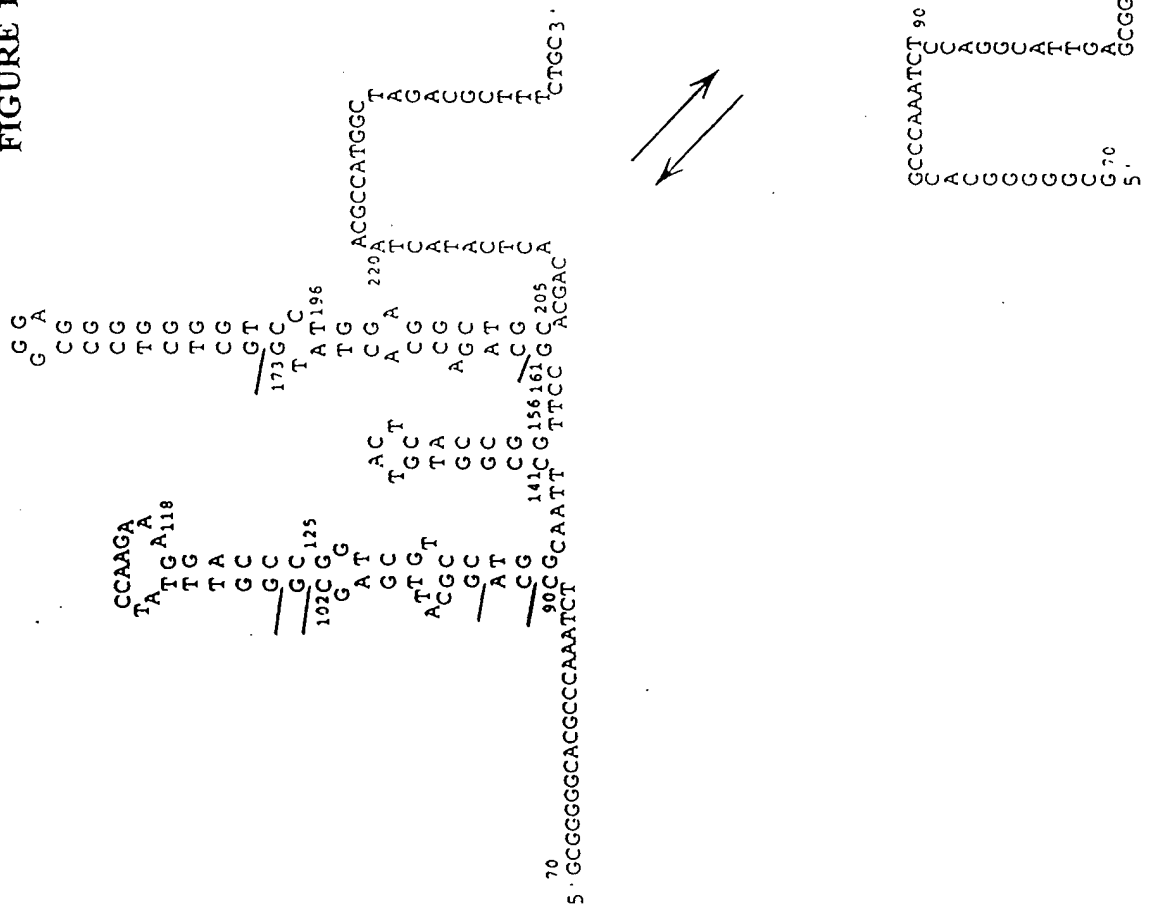


FIGURE 17B



5' Biotin—AAATCT 141CG¹⁵⁶¹⁶¹GC²⁰⁵ACGACACT—3'
 (179-49-01)3'—GGCCAAGGTTTGCTGTGA—Fl-5'
 (#81-01)3'—TTAA^{TT}AAGG^{TT}TGCTGTGA—Fl-5'

5' Biotin ——— TCCAAGAA GGAGGCTG ——— 3'
m (#81-04) 3' ——— AGGTTCTT CC CCTCCGAC ——— Fl-5'

FIGURE 18A

HCV 1a

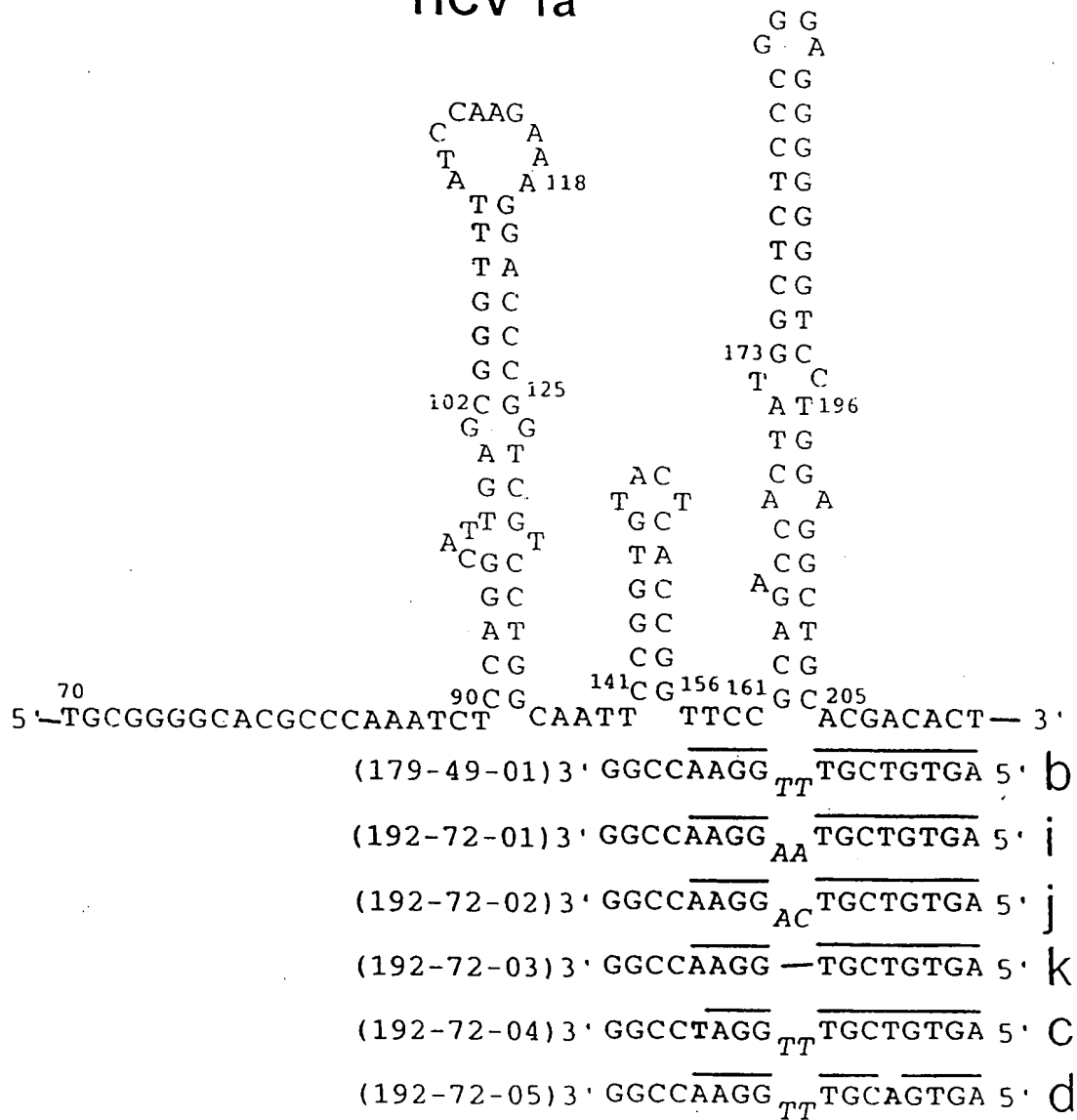


FIGURE 18B

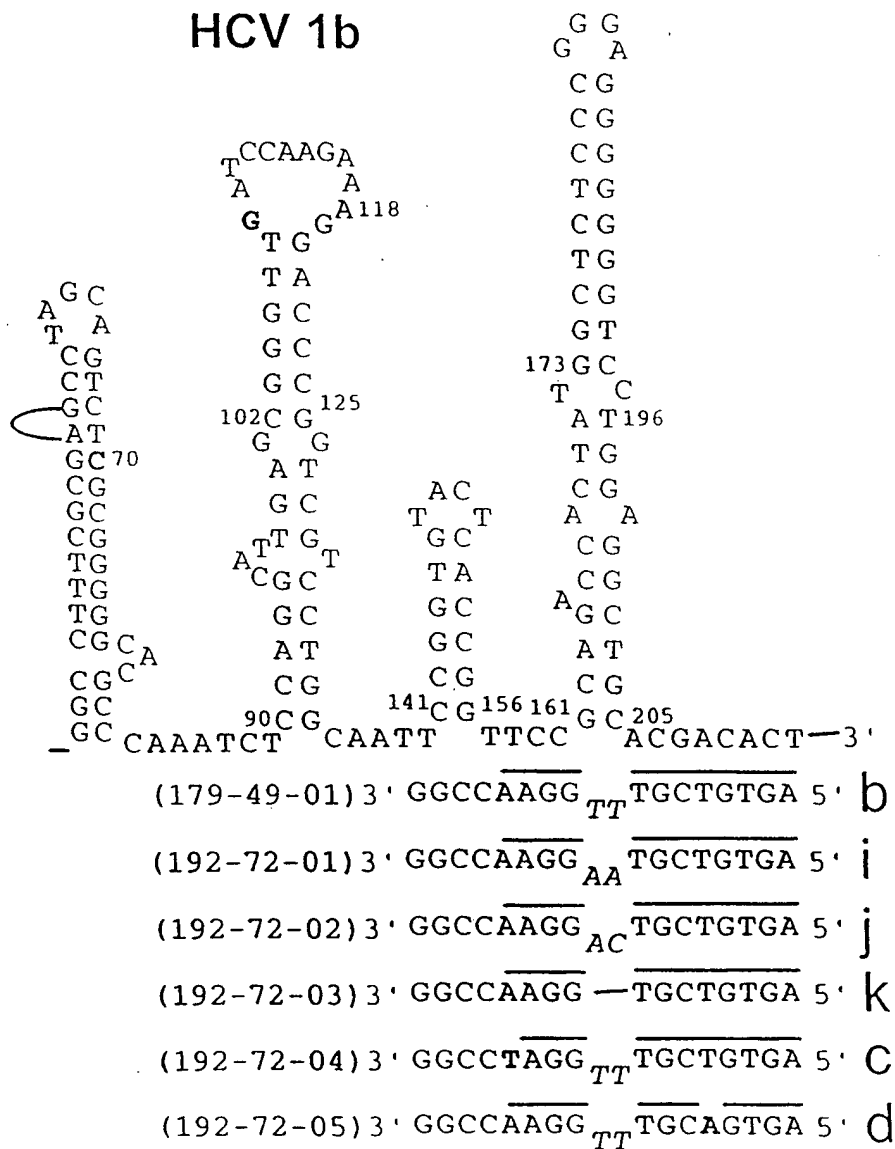


FIGURE 18C

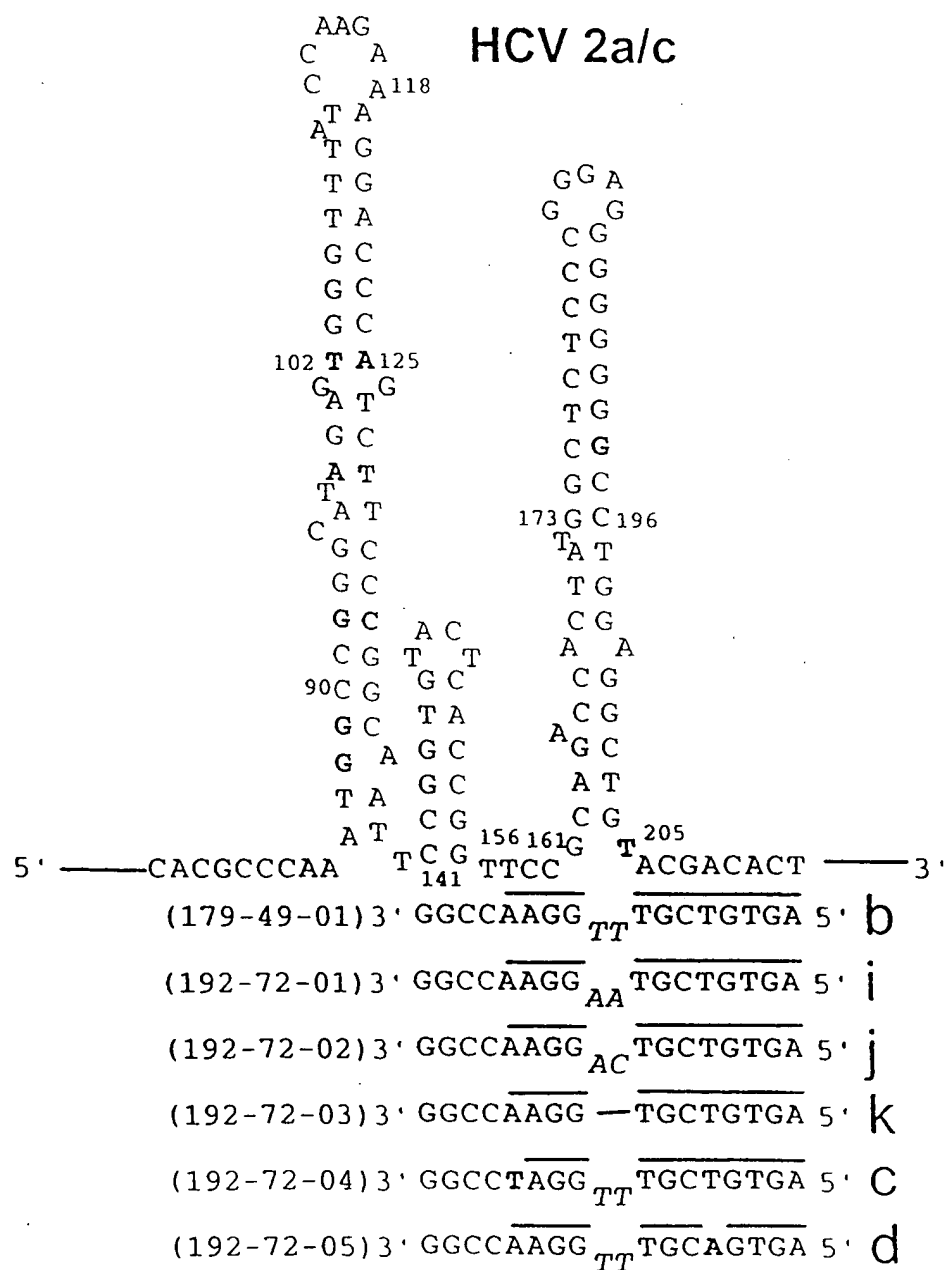


FIGURE 18D

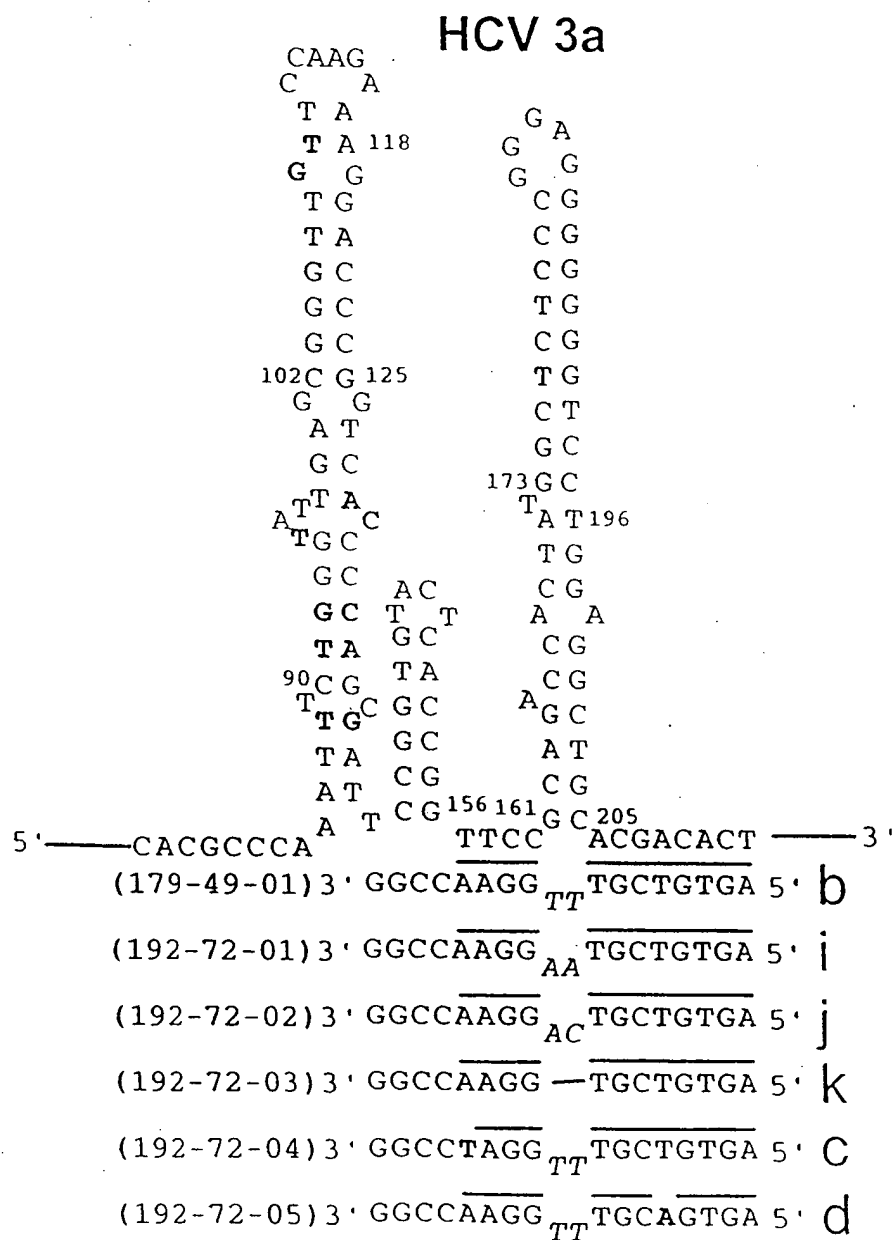


FIGURE 19

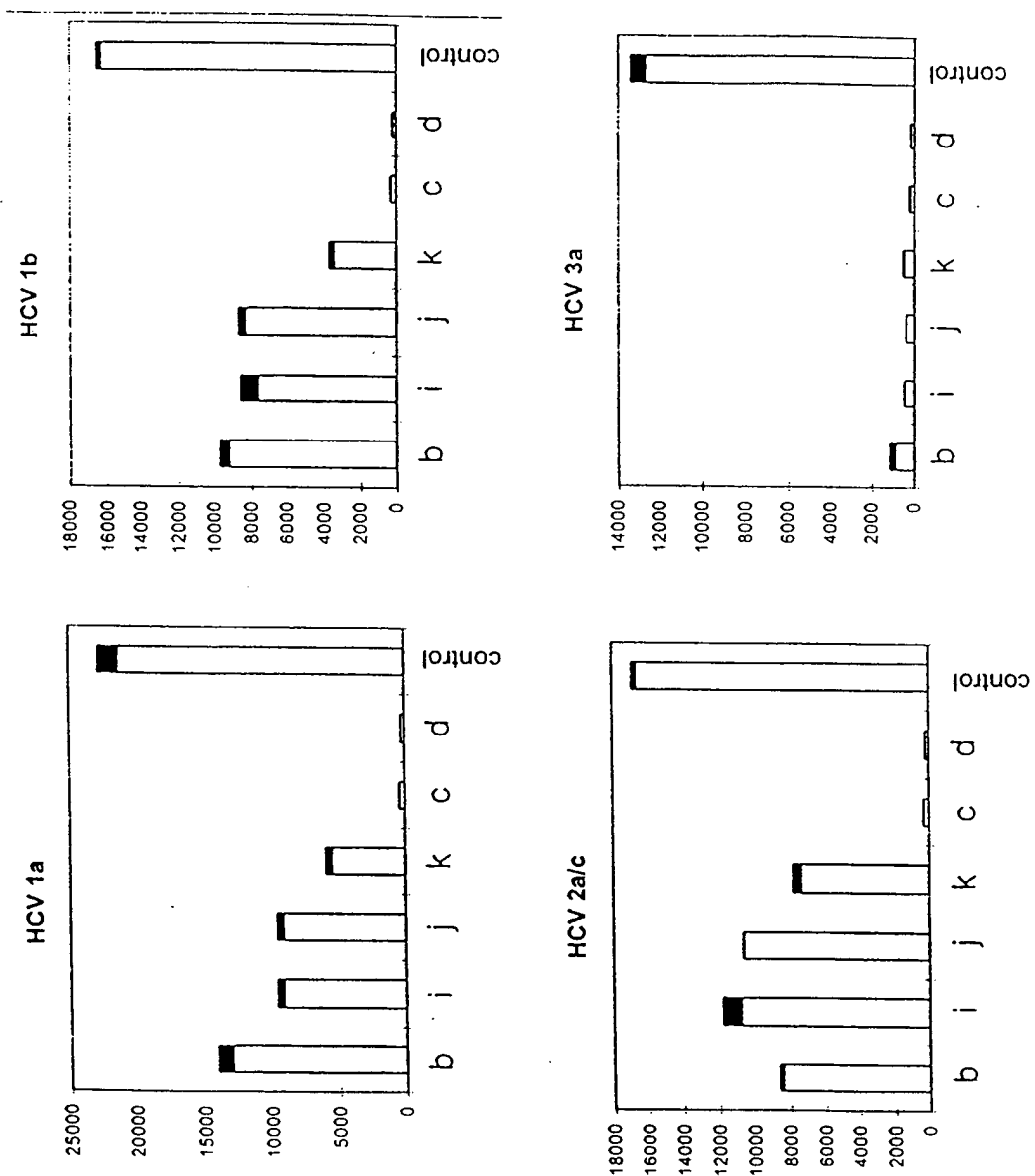
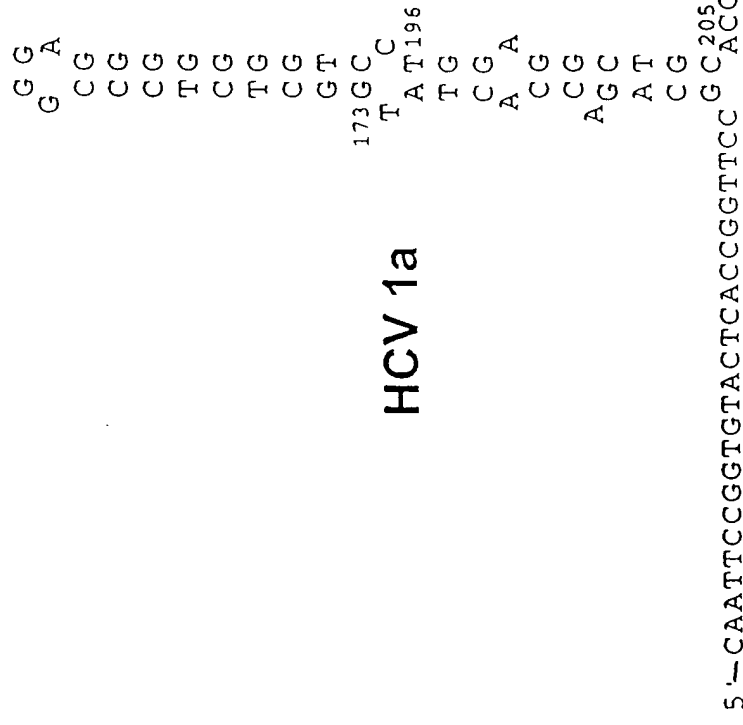
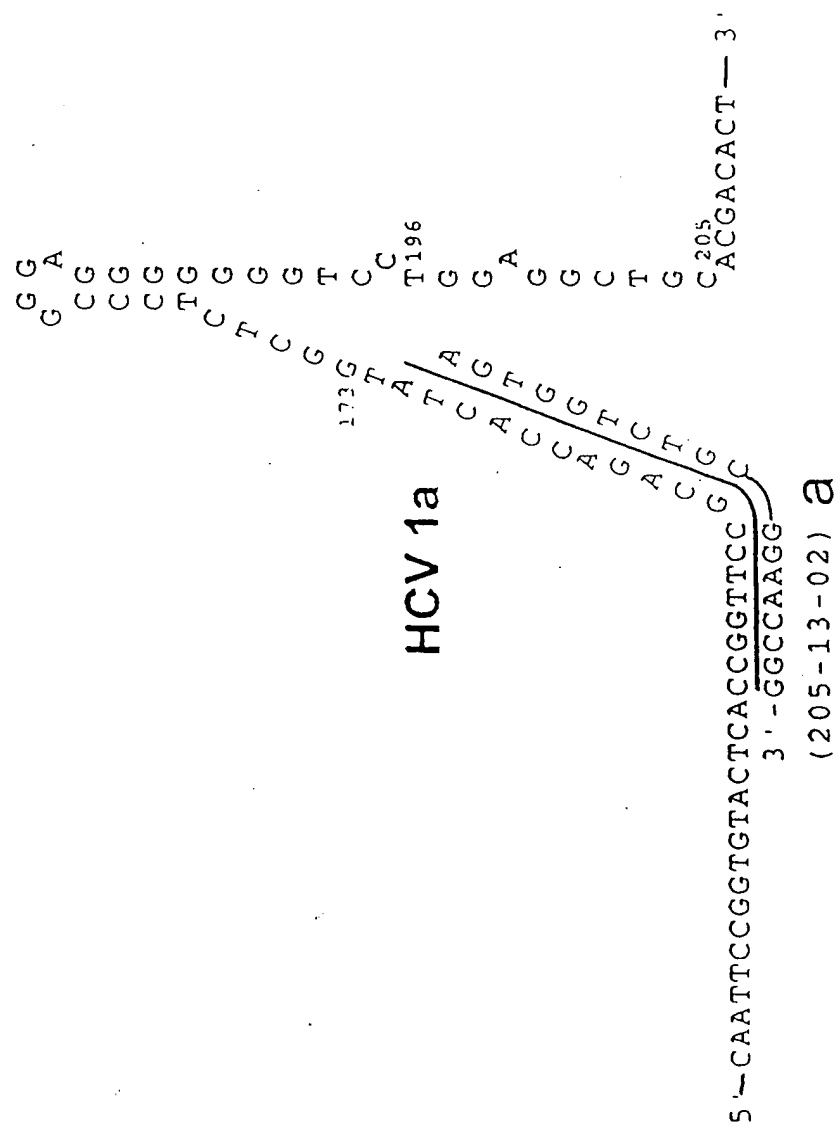


FIGURE 20A



- a 3'-GGCCAAAGGCGTCTGGTGA-F1'5' (205-13-02)
- b 3'-GGCCAAAGG_{TT}TGCTGTGA-F1'5' (179-49-01)
- c 3'-GGCCCTAGG_{TT}TGCTGTGA-F1'5' (192-72-04)
- d 3'-GGCCAAAGG_{TT}TGCCAGTGA F1'5' (192-72-05)
- e 3'-GGCCAAAGG-F15' (205-27-01)

FIGURE 20B



G G A
 C G
 C G
 C G
 T G
 C G
 T G
 C G
 G T
 173 G C C
 T A T¹⁹⁶
 T G
 C G
 A A
 C G
 C G
 A G C
 A T
 C G
 G C²⁰⁵
 5'-CAATTCCGGTGTA^{CT}CACCGGTTCC

HCV 1a

5'-CAATTCGGTGTA^{C205}CTACCGGTCCG^CACGACACT-3'

3' - GGCCAAGCGTCTGGTGA - F1' 5' (205-13-02) a

3' - GGCCAAGG TGCTGTGA...Fl' 5' (179-49-01) b

3' - GGCCAAGG - F15' (205-27-01)

FIGURE 23

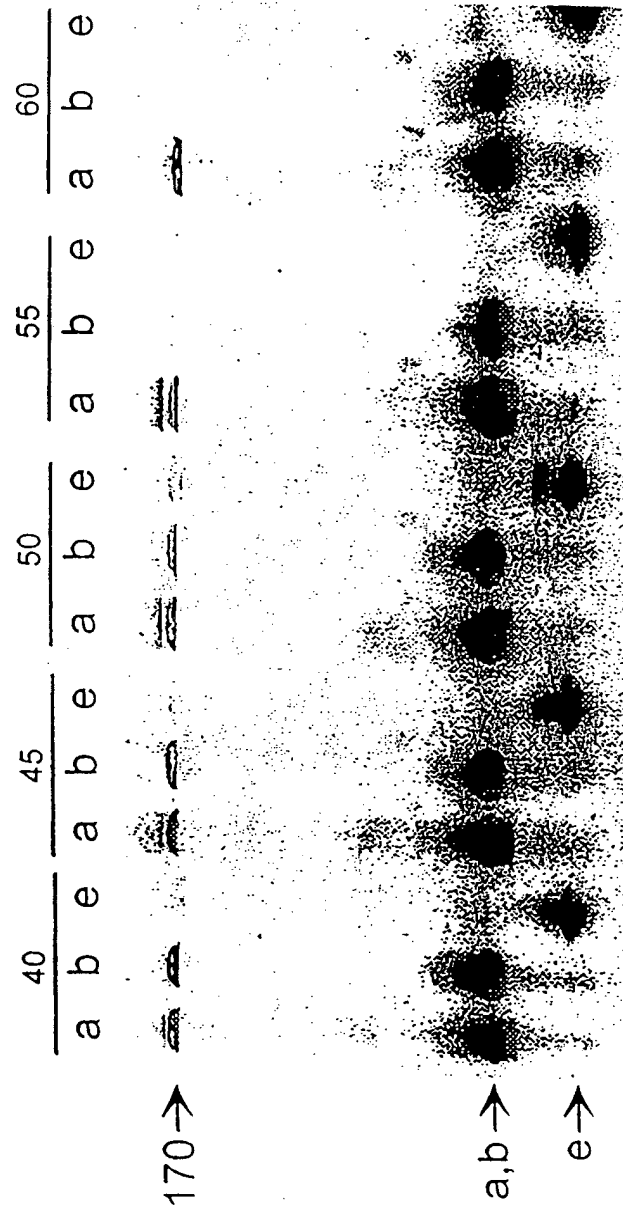


FIGURE 24

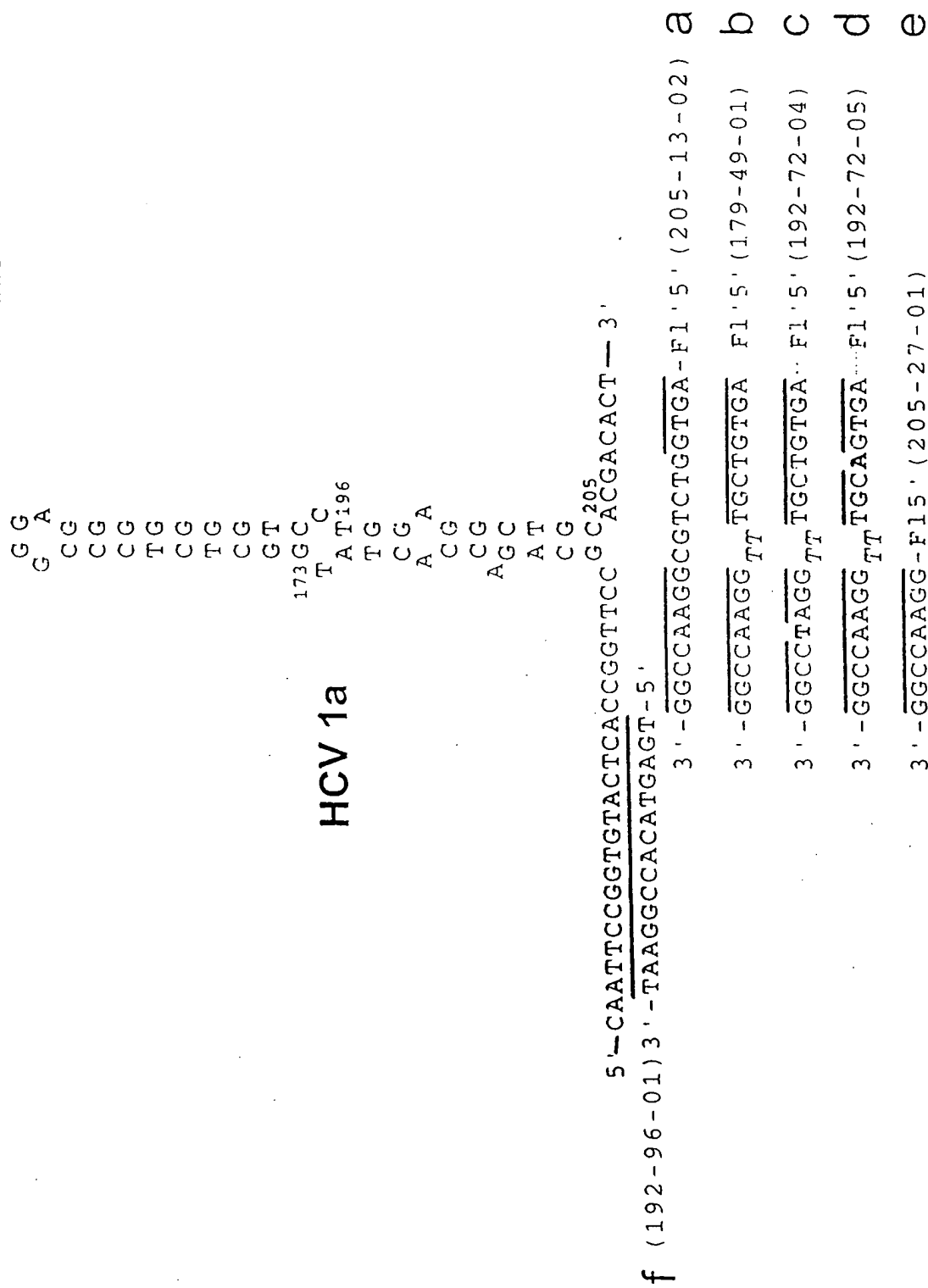


FIGURE 25

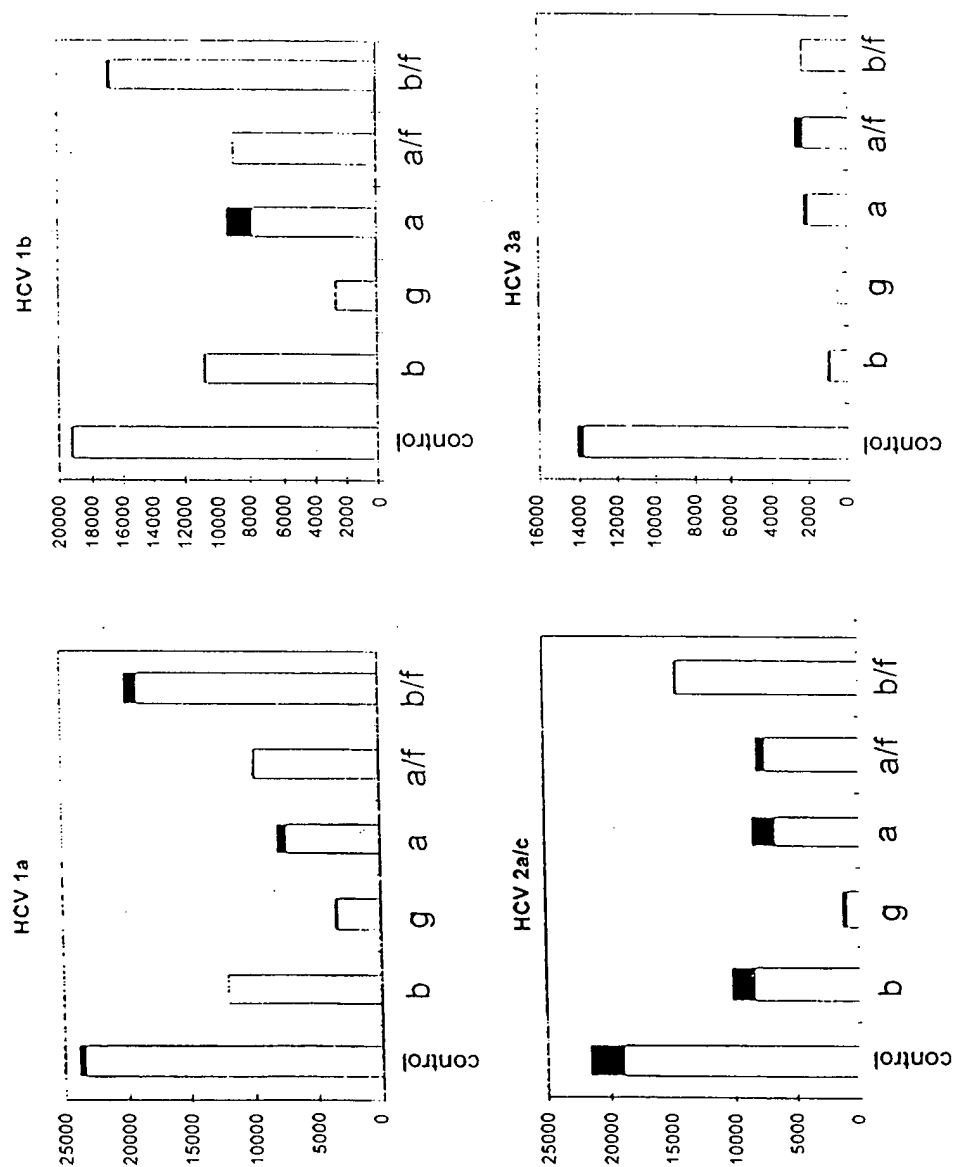


FIGURE 26

5'-ATTCCGGTGTACTCACCGGTTCAAACGACACT-3' (205-13-01) S.T.
 f (192-96-01) 3'-TAAGGCCACATGAGT-5'
 3'-GGCCAAAGCGCTCTGGTGA-F1'5' (205-13-02) a
 3'-GGCCAAAGG_{TT}TGCTGTGA---F1'5' (179-49-01) b
 3'-GGCCTAGG_{TT}TGCTGTGA---F1'5' (192-72-04) c
 3'-GGCCAAAGG_{TT}TGCAGTGA F1'5' (192-72-05) d
 3'-GGCCAAAGG-F15' (205-27-01) e

FIGURE 27

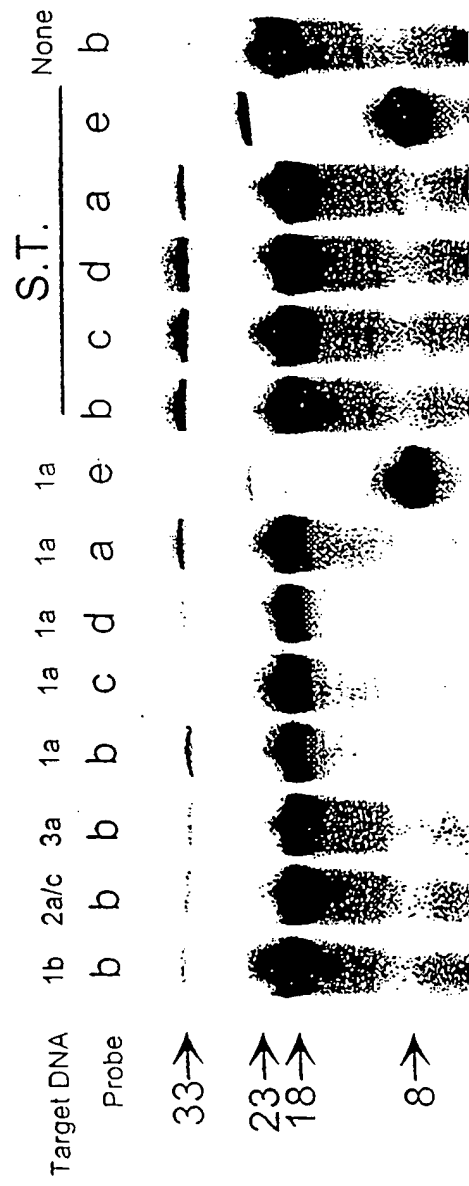


FIGURE 28

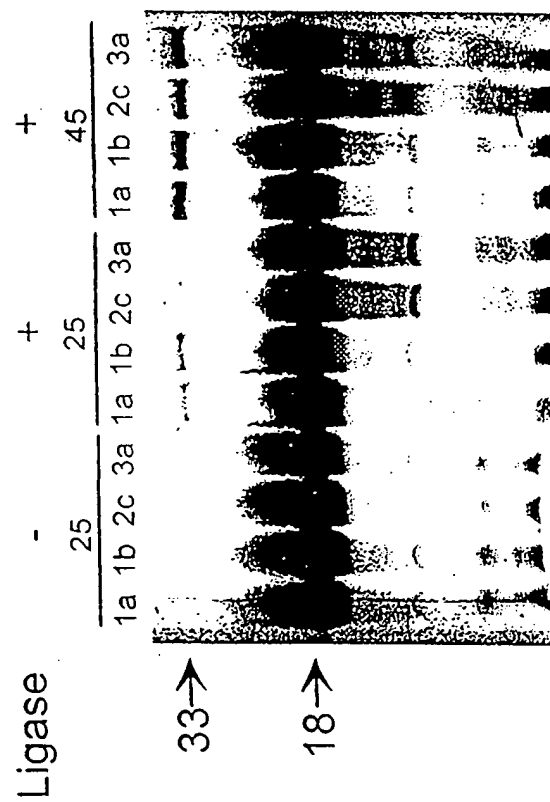


FIGURE 29A

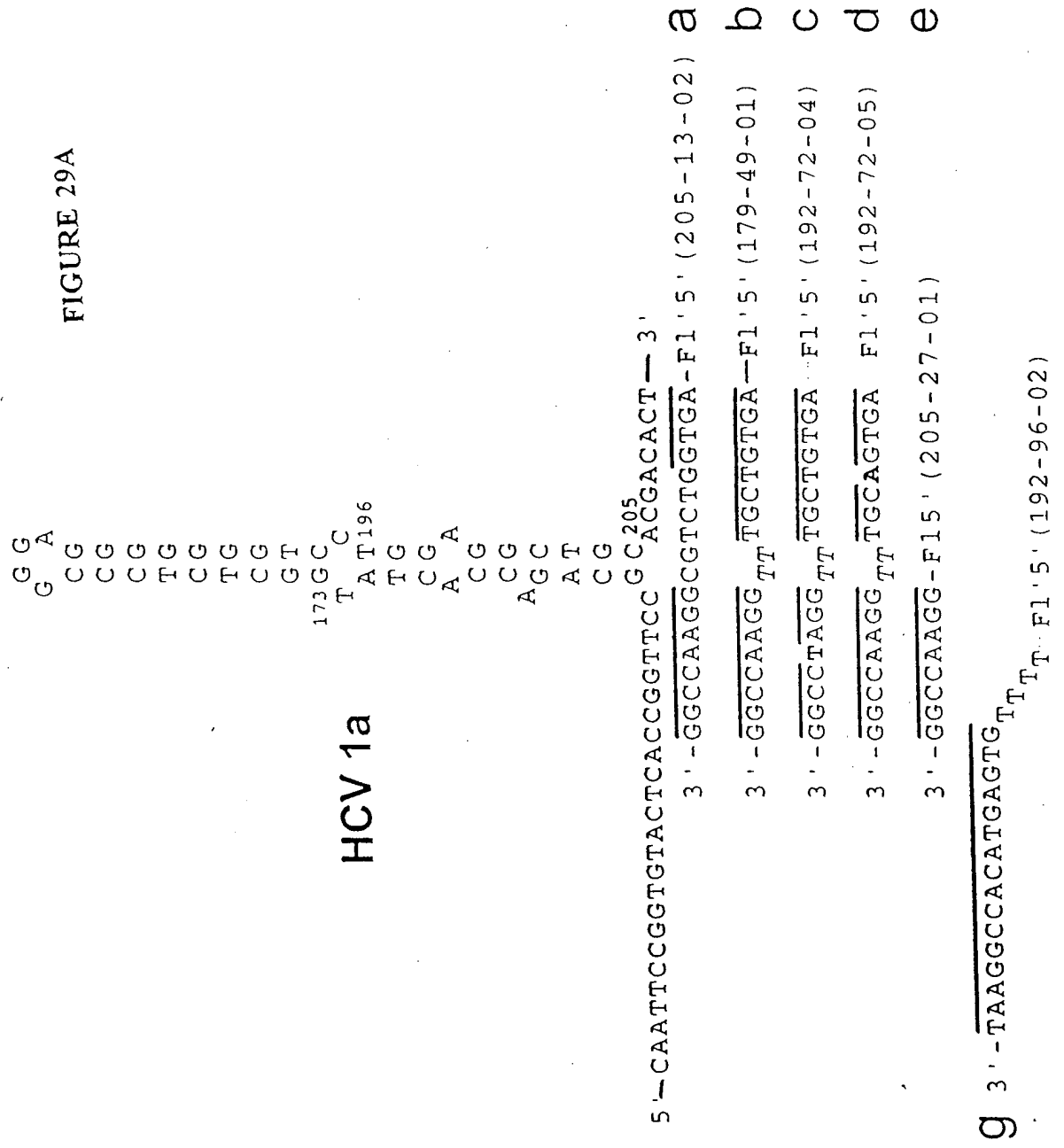


FIGURE 29B

5' -ATTCCGGTGTACTCACC GGTTCCAAACGACACT-3' (205-13-01) S.T.

3' -GGCCAAAGCGCTCTGGTGA-F1'5' (205-13-02) a

3' -GGCCAAAGG_{TT} TGCTGTGA--F1'5' (179-49-01) b

3' -GGCCTAGG_{TT} TGCTGTGA--F1'5' (192-72-04) c

3' -GGCCAAAGG_{TT} TGCAGTGA--F1'5' (192-72-05) d

3' -GGCCAAAGG-F15' (205-27-01) e

g 3' -TAAGGCCACATGAGTG_T T_T--F1'5' (192-96-02)

FIGURE 30

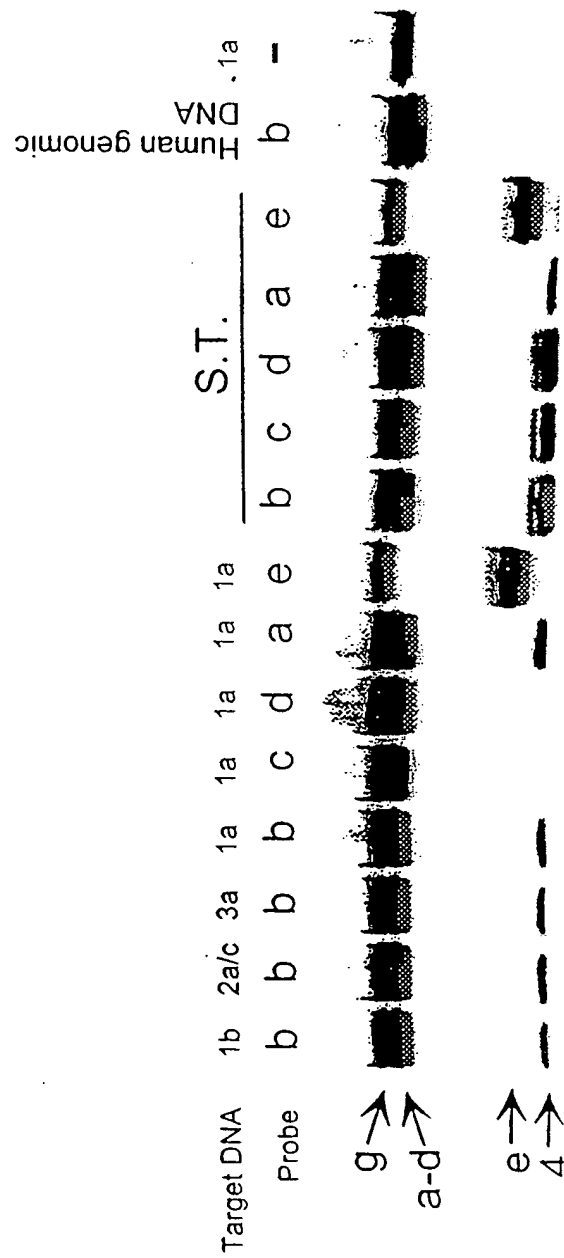


FIGURE 31

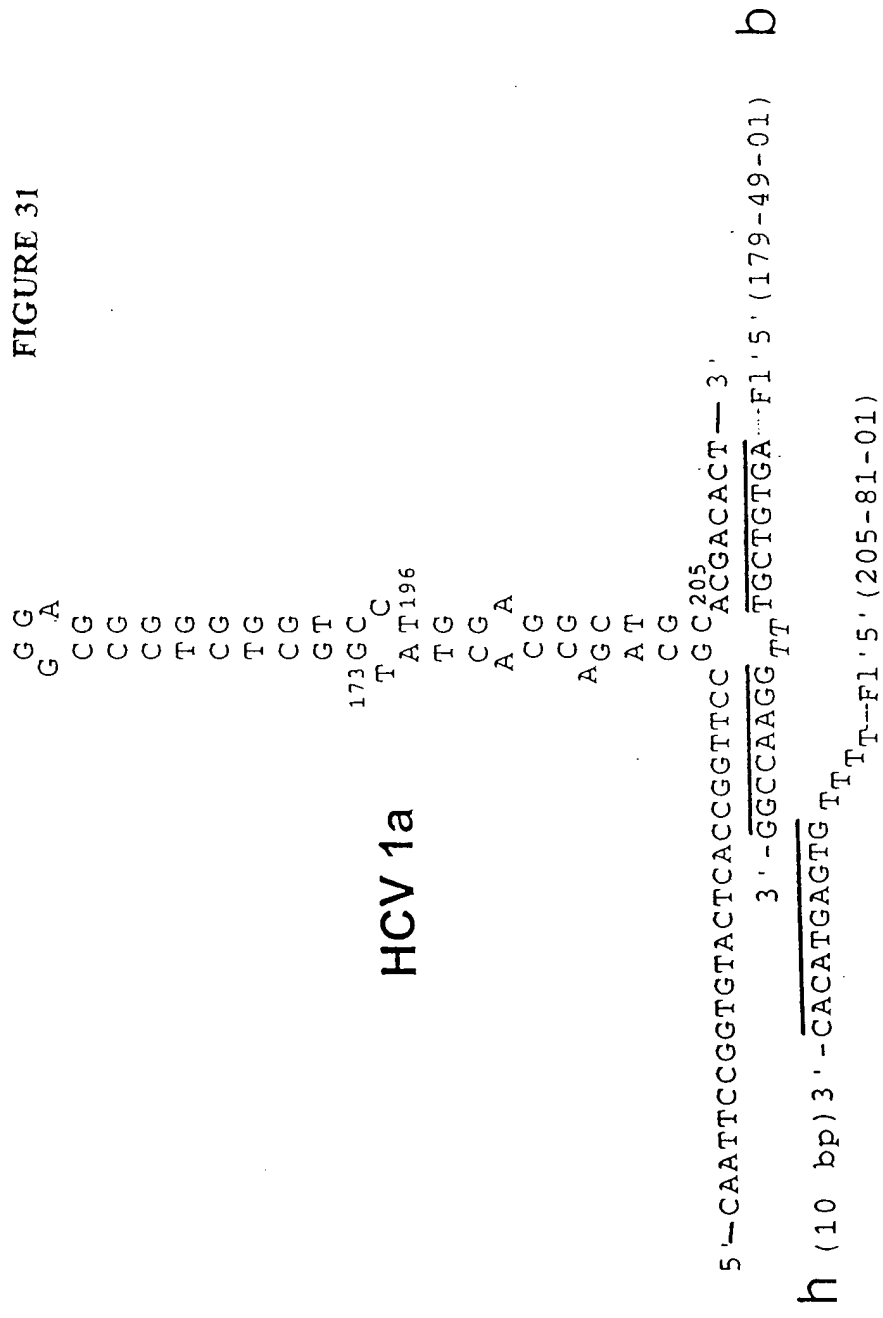


FIGURE 32

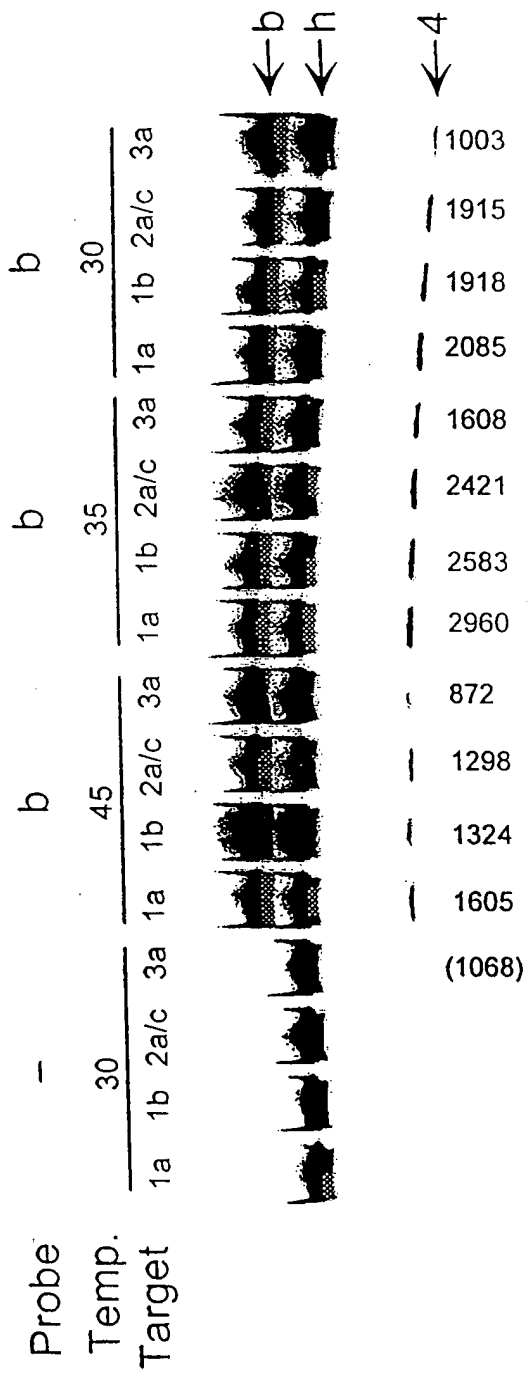


FIGURE 33

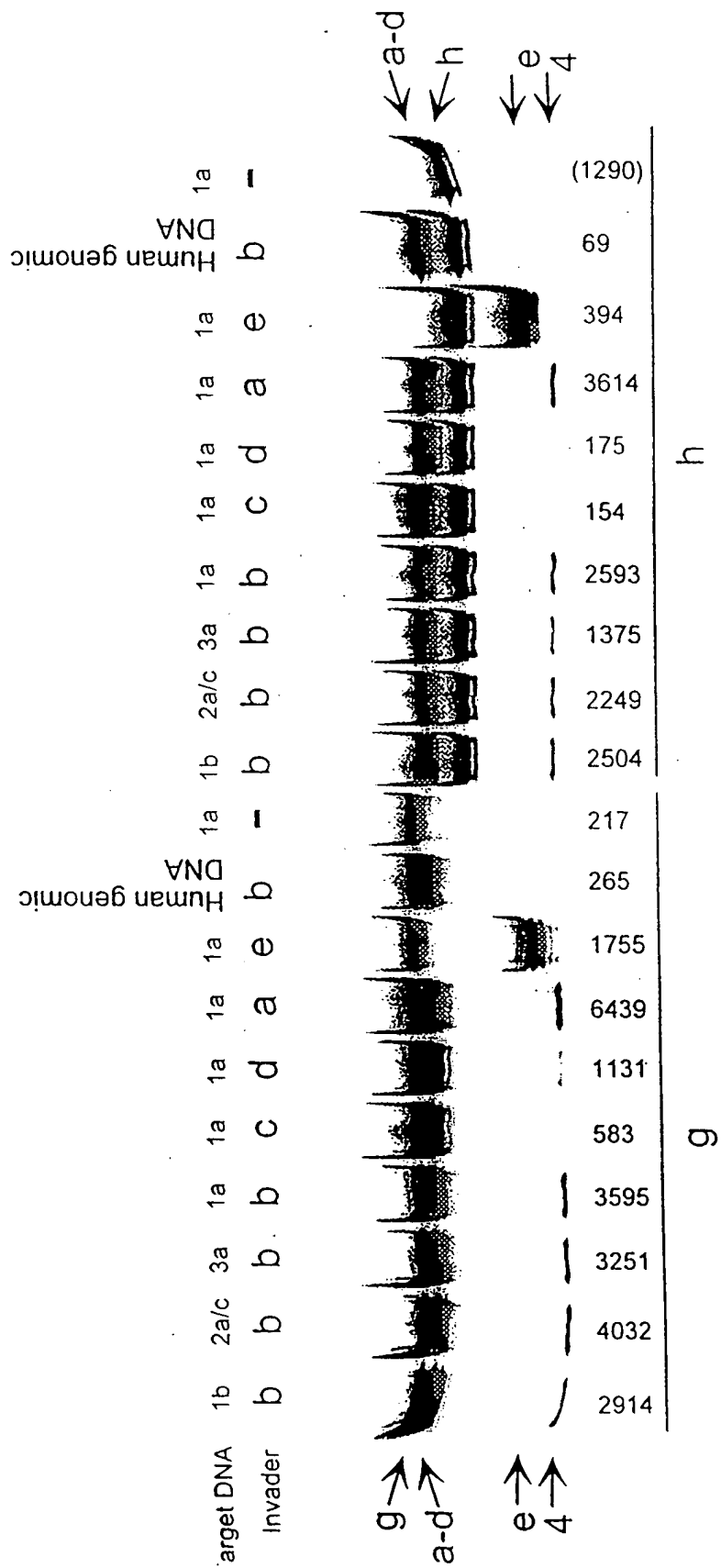
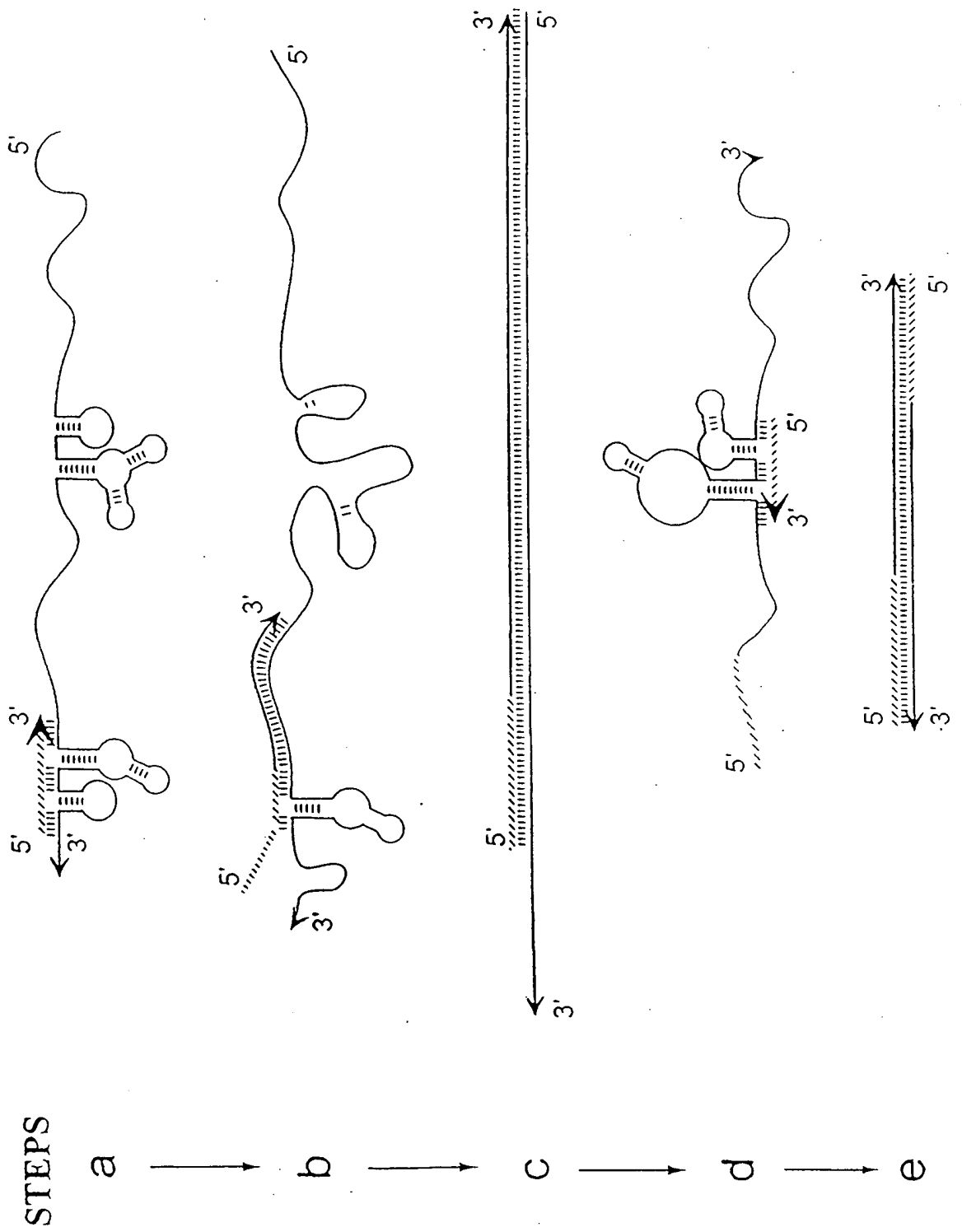


FIGURE 34



STEPS

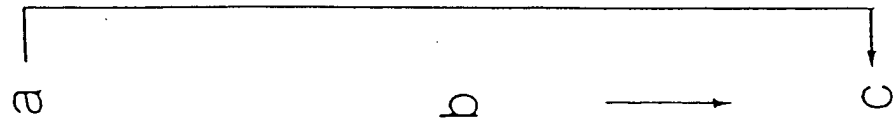


FIGURE 35

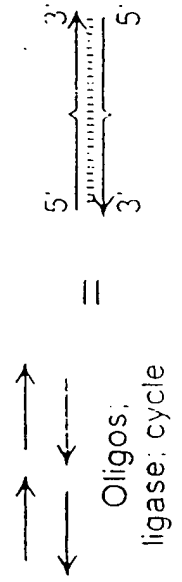
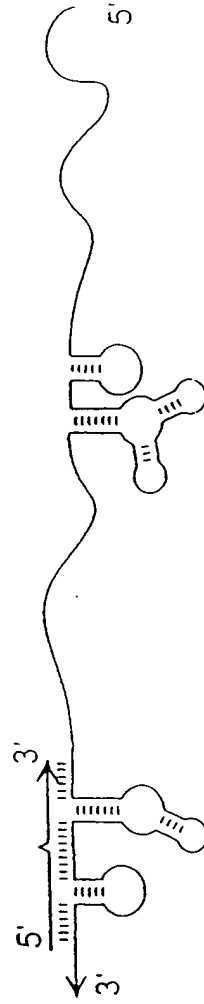
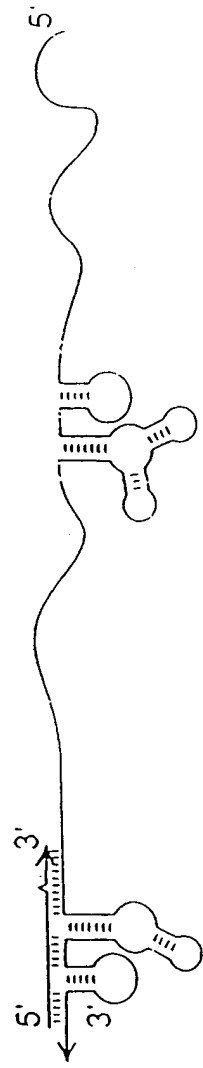


FIGURE 36

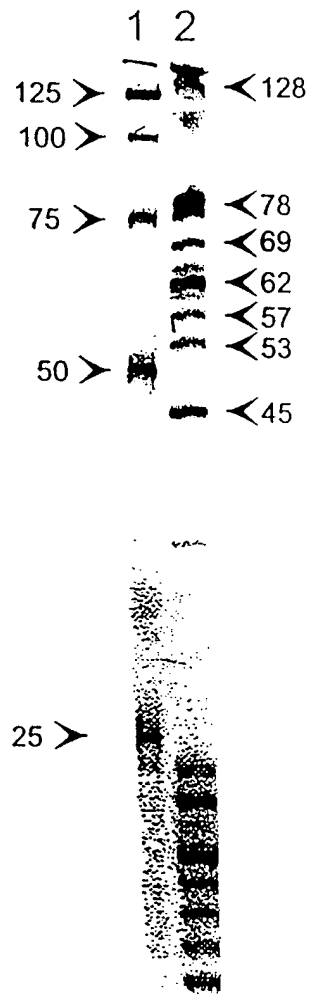


FIGURE 37A

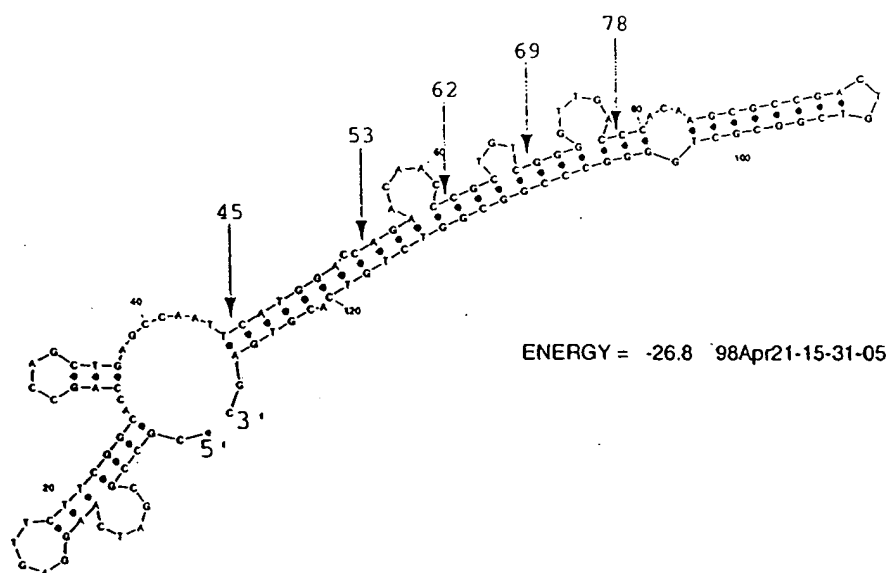
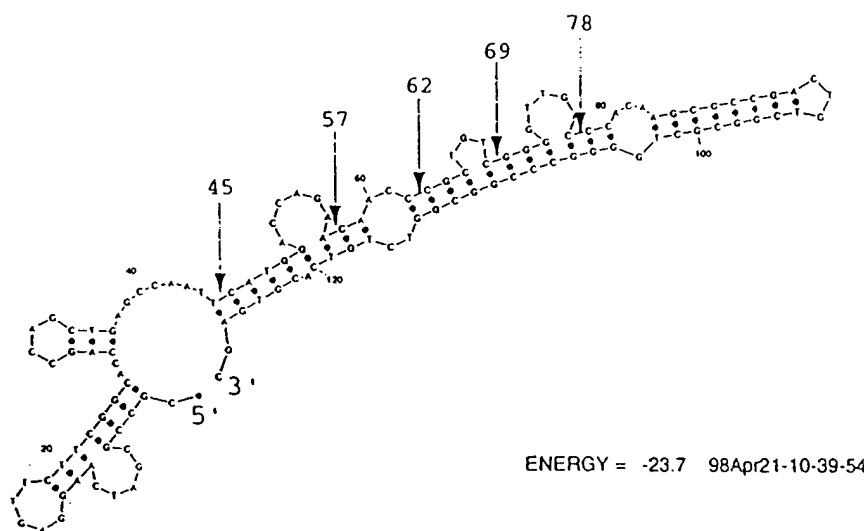


FIGURE 37B

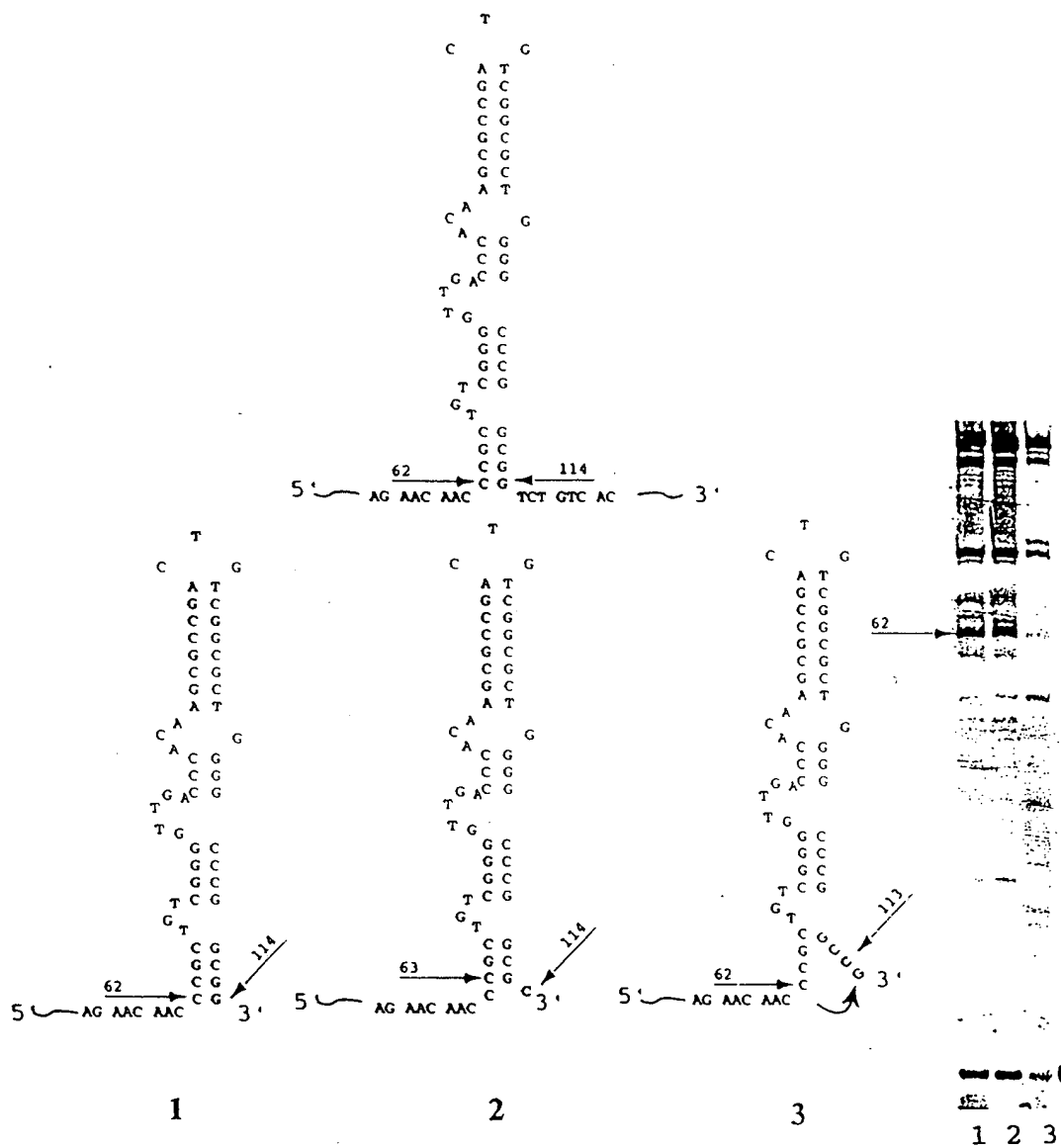


FIGURE 37C

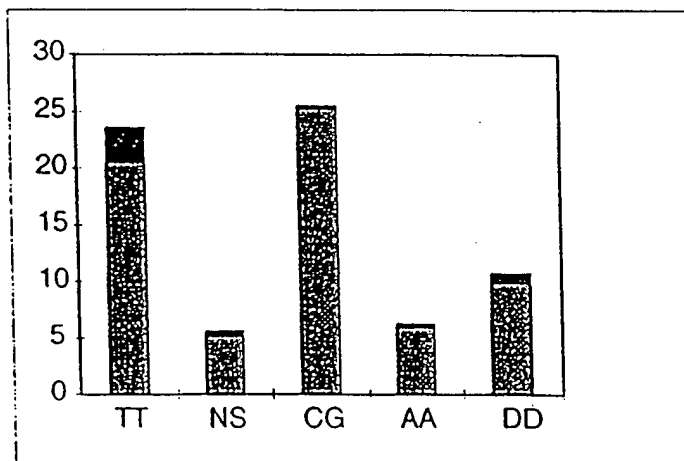
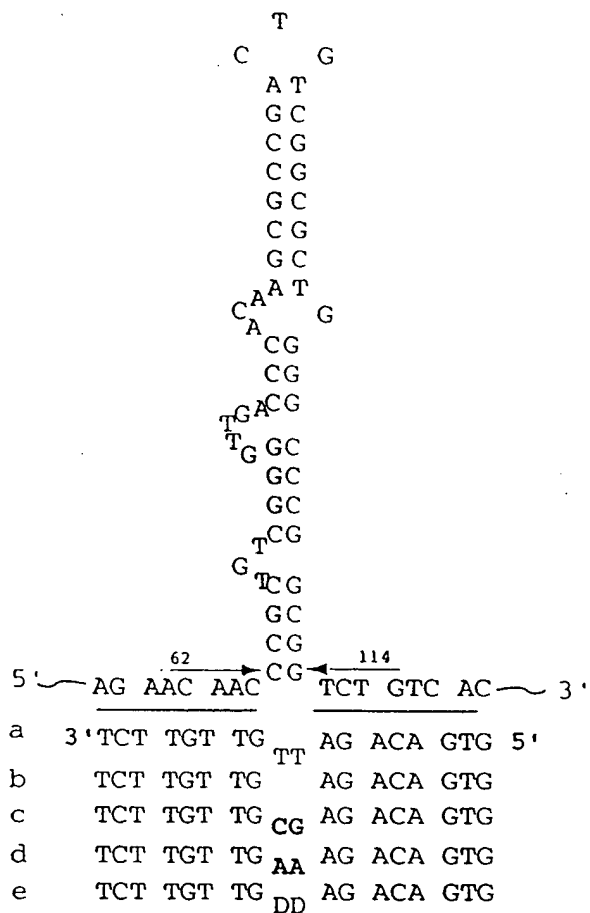


FIGURE 38A

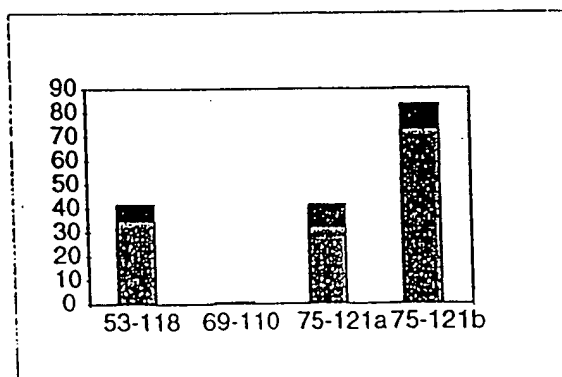
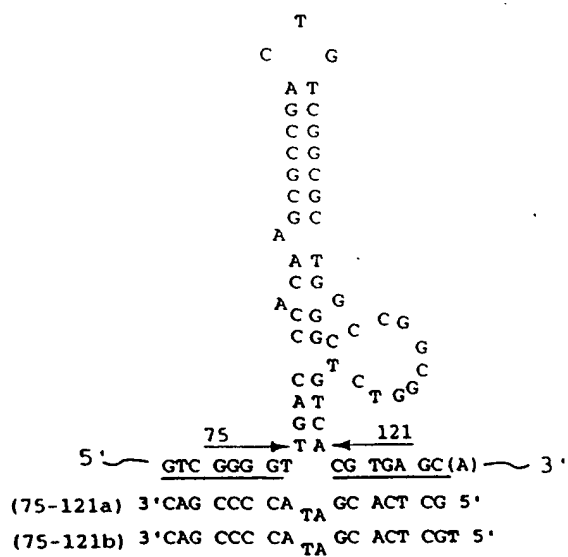
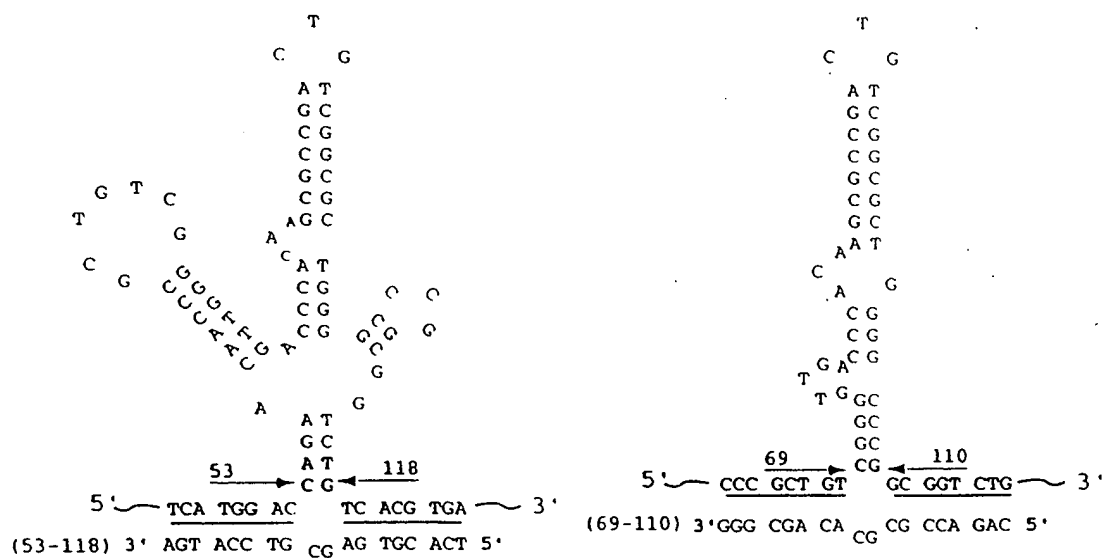


FIGURE 38B

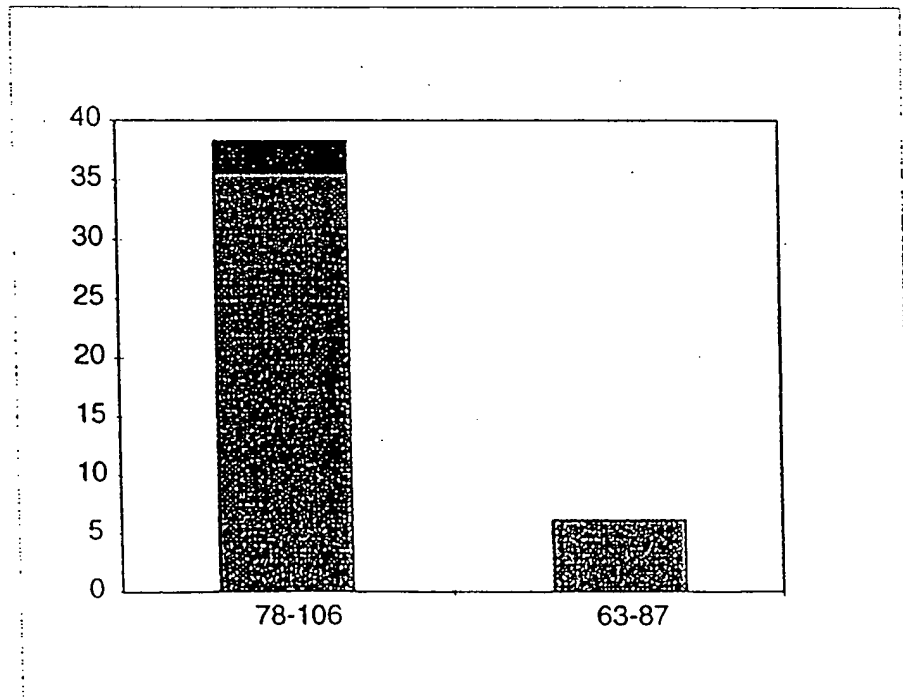
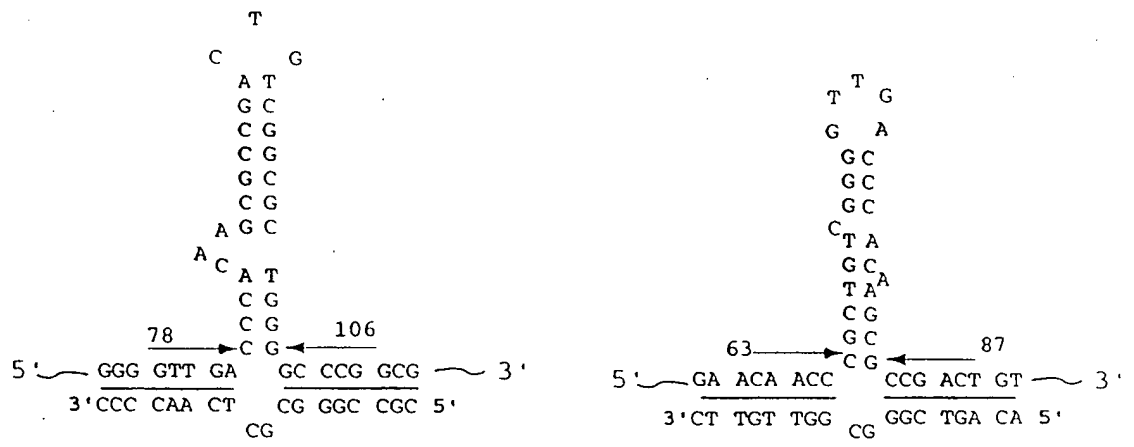
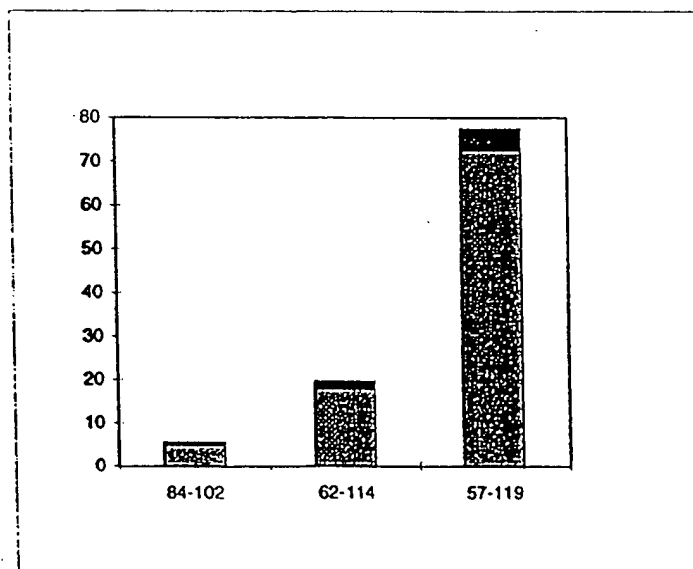
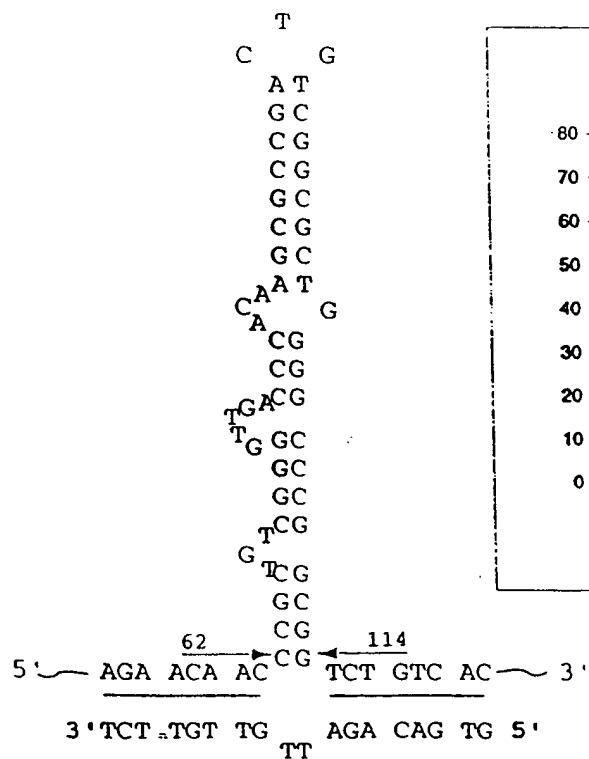
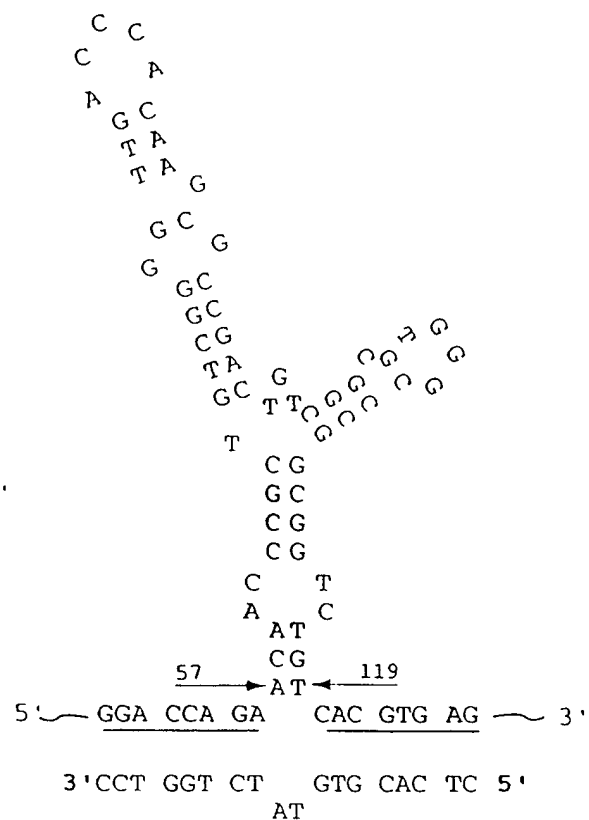
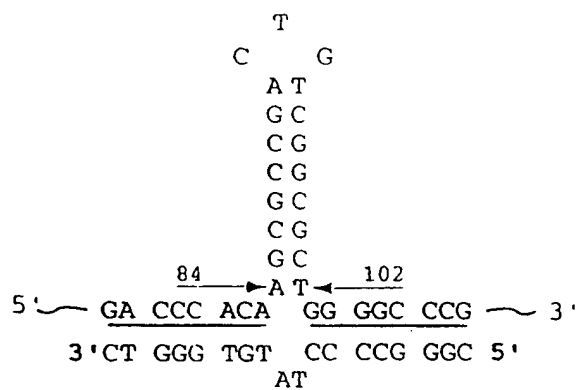


FIGURE 38C



	T	
C		G
A	T	
G	C	
C	G	
C	G	
G	C	
C	G	
G	C	
A	T	

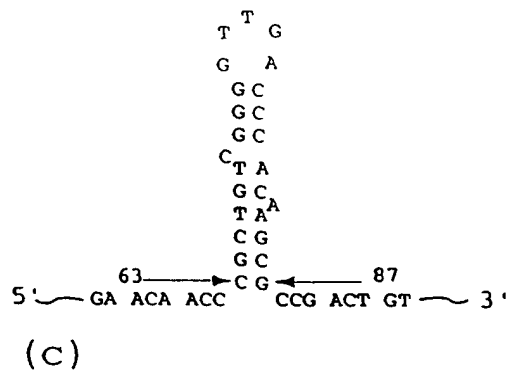


FIGURE 40

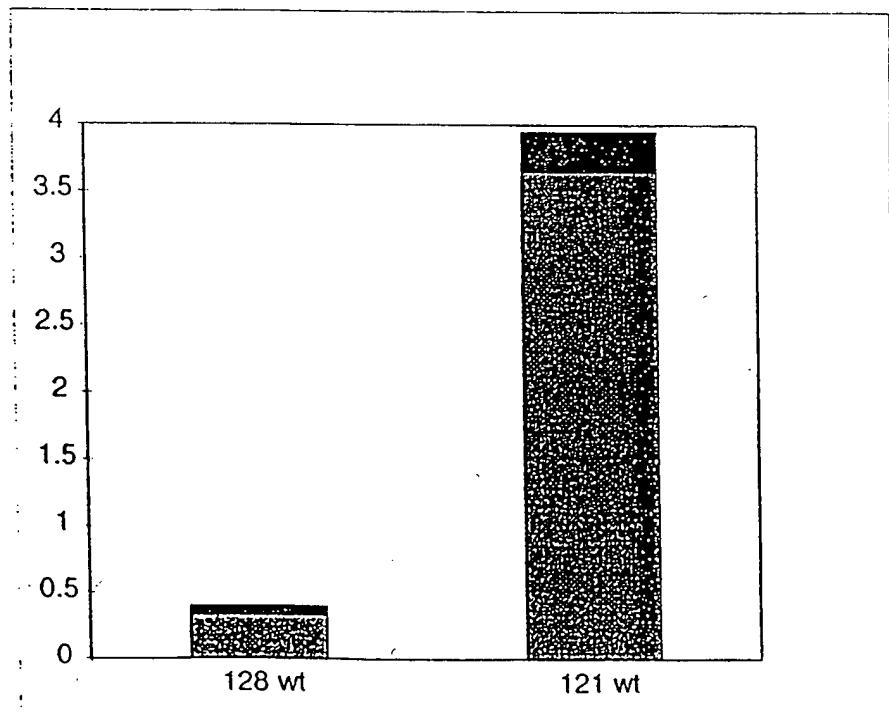
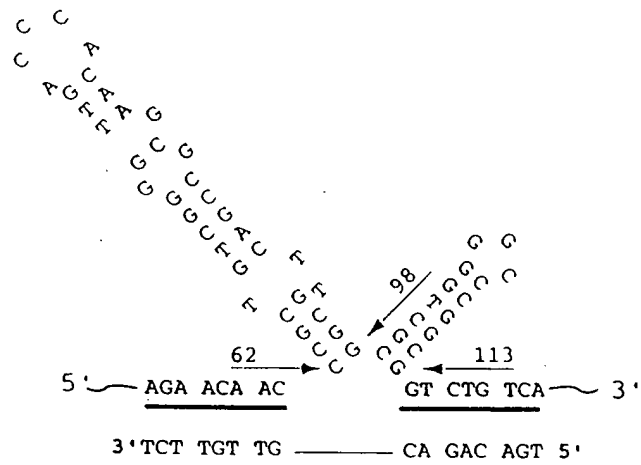


FIGURE 41

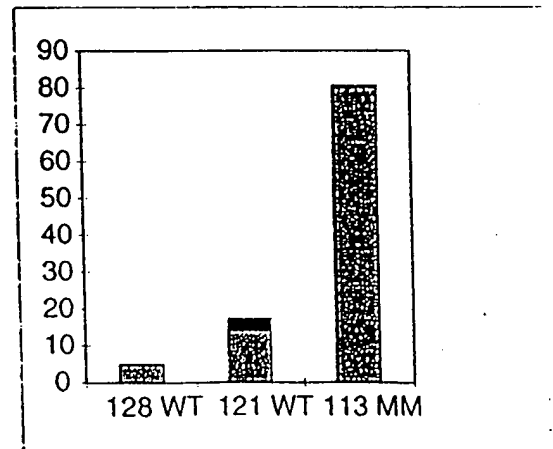
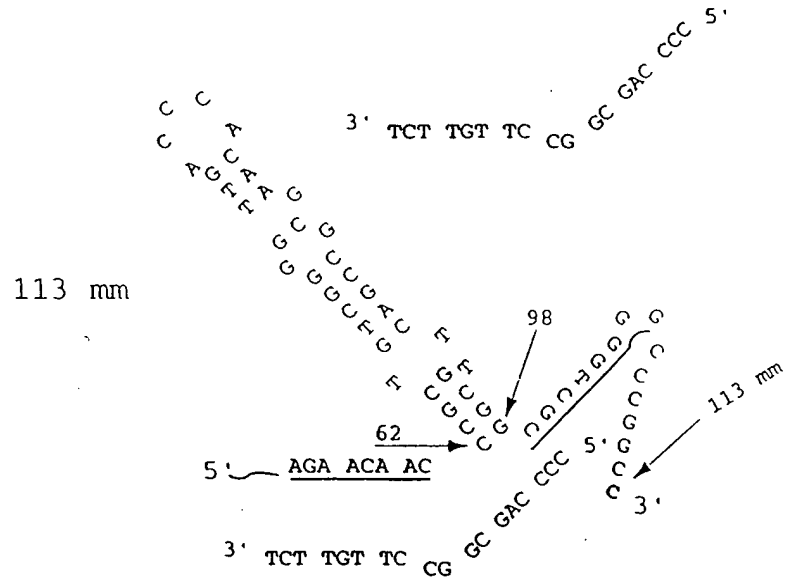
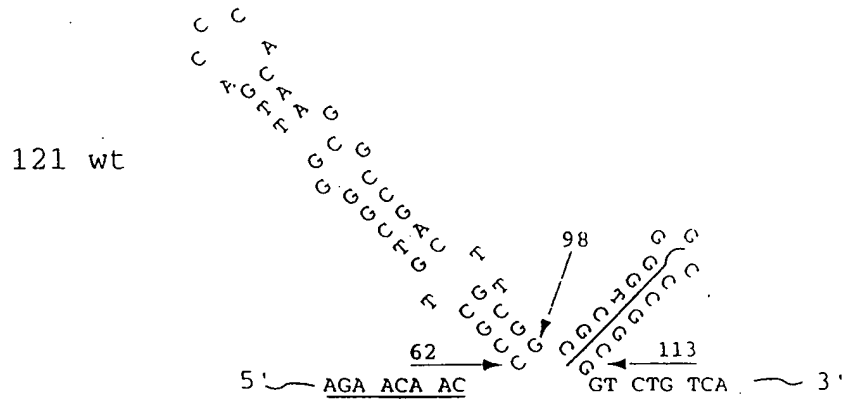


FIGURE 42

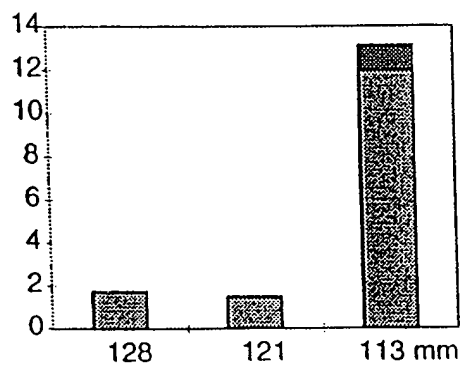
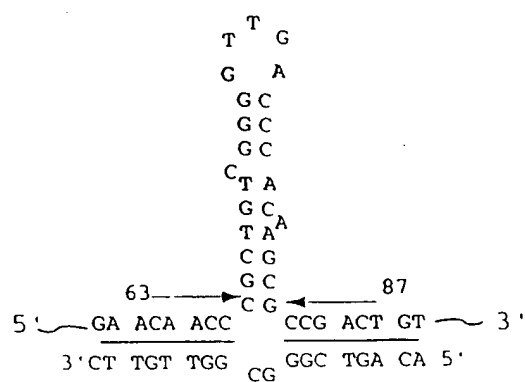


FIGURE 43A

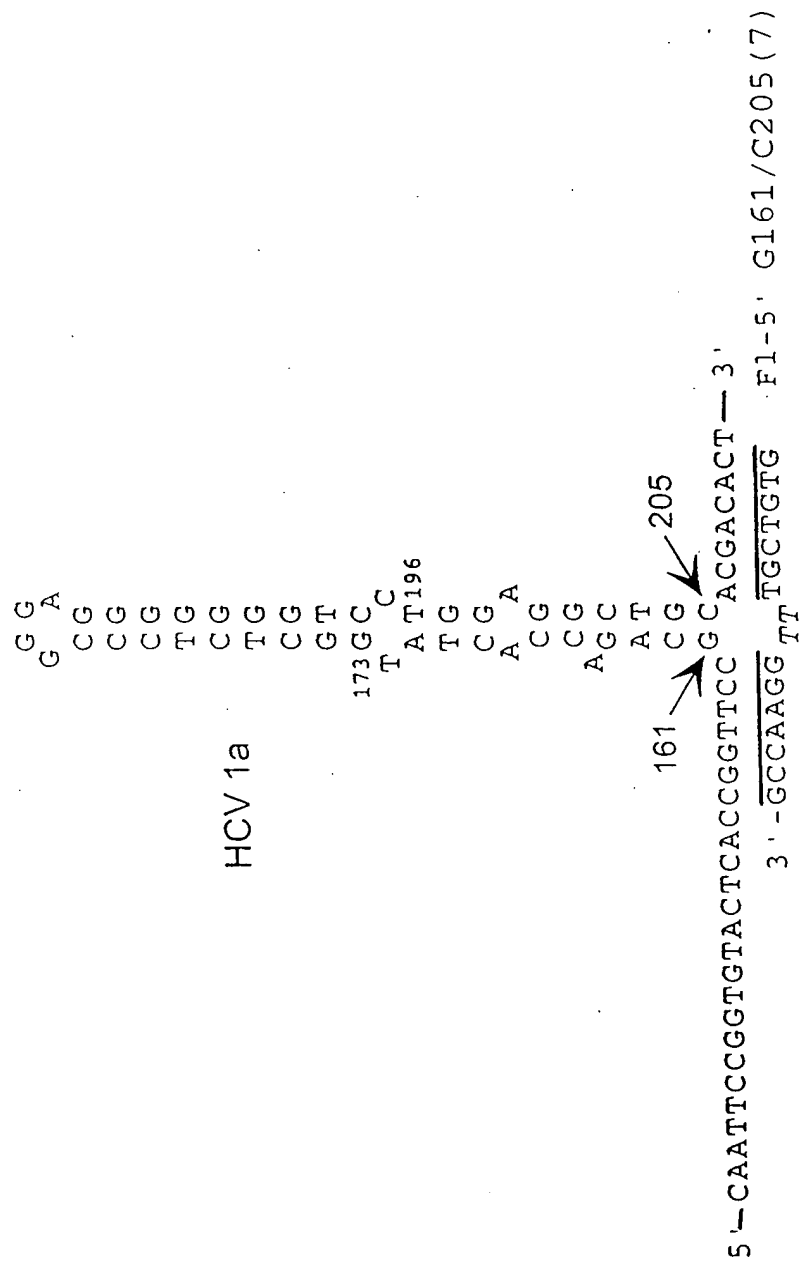


FIGURE 43B

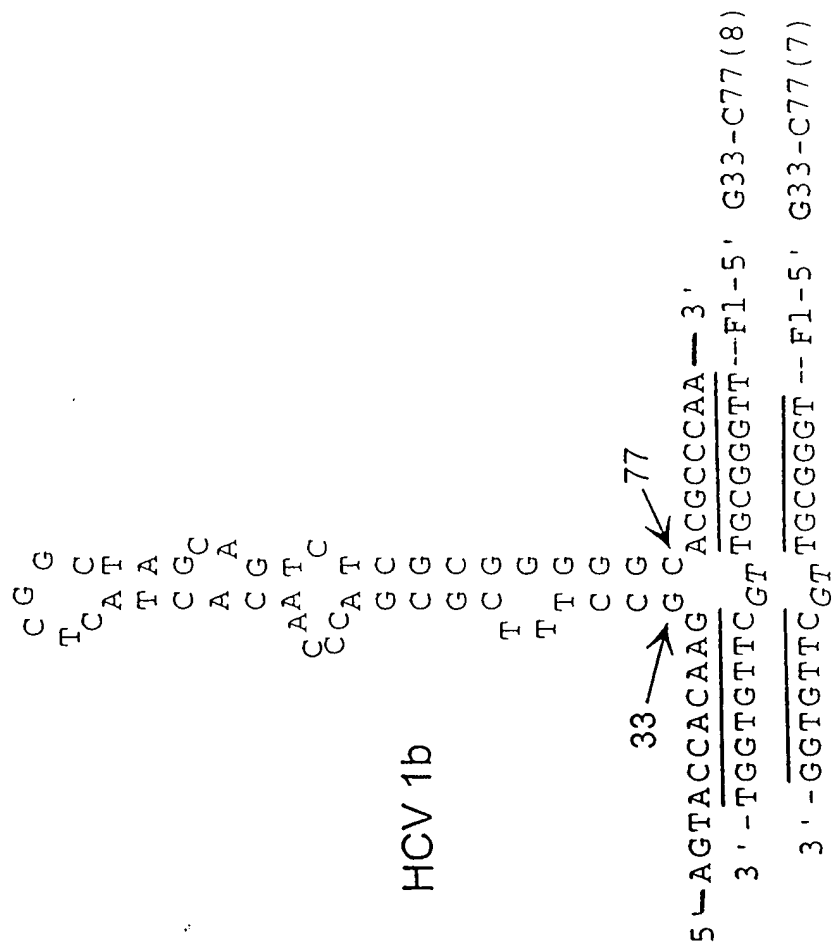


FIGURE 44A

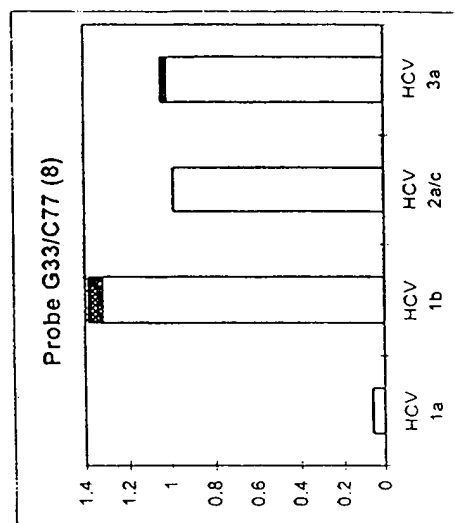
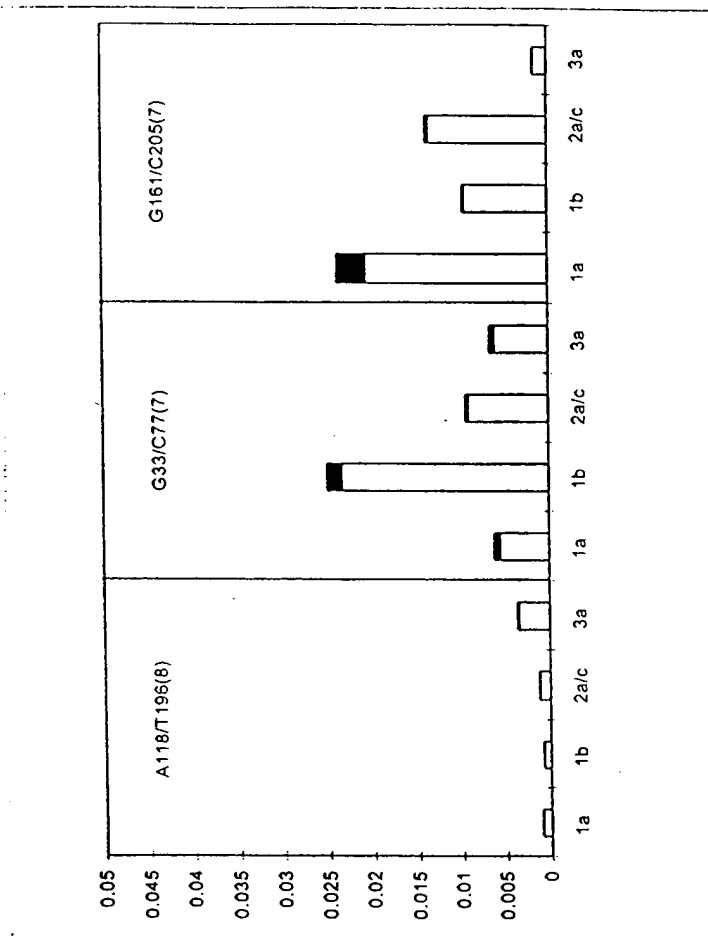


FIGURE 44B



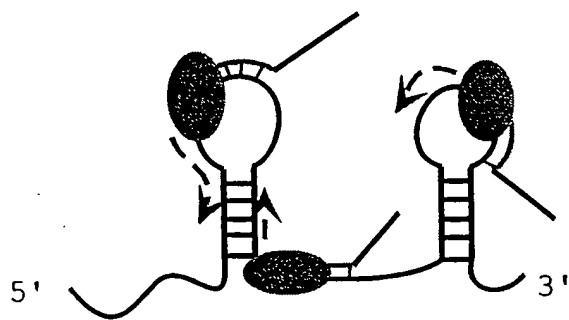
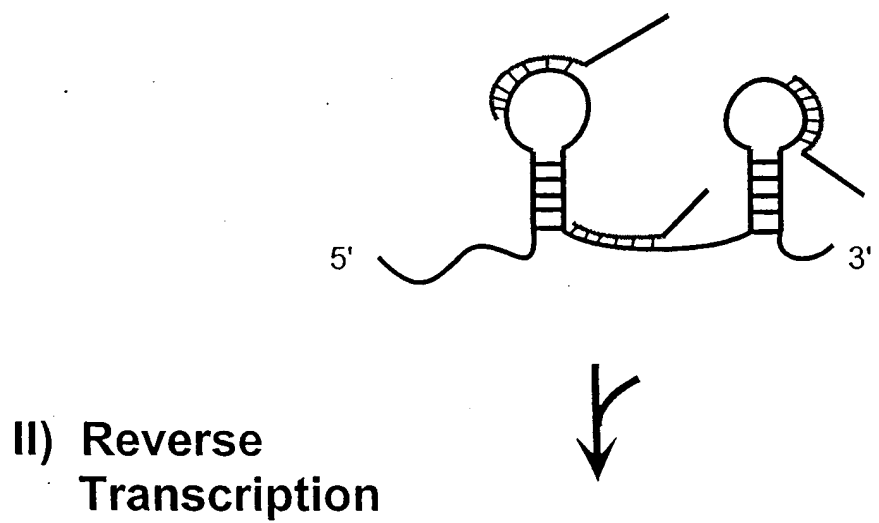
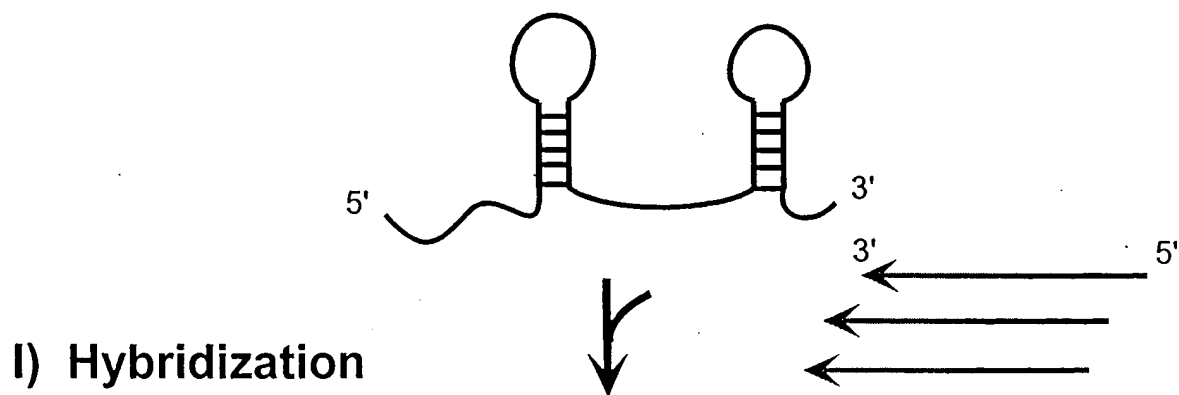
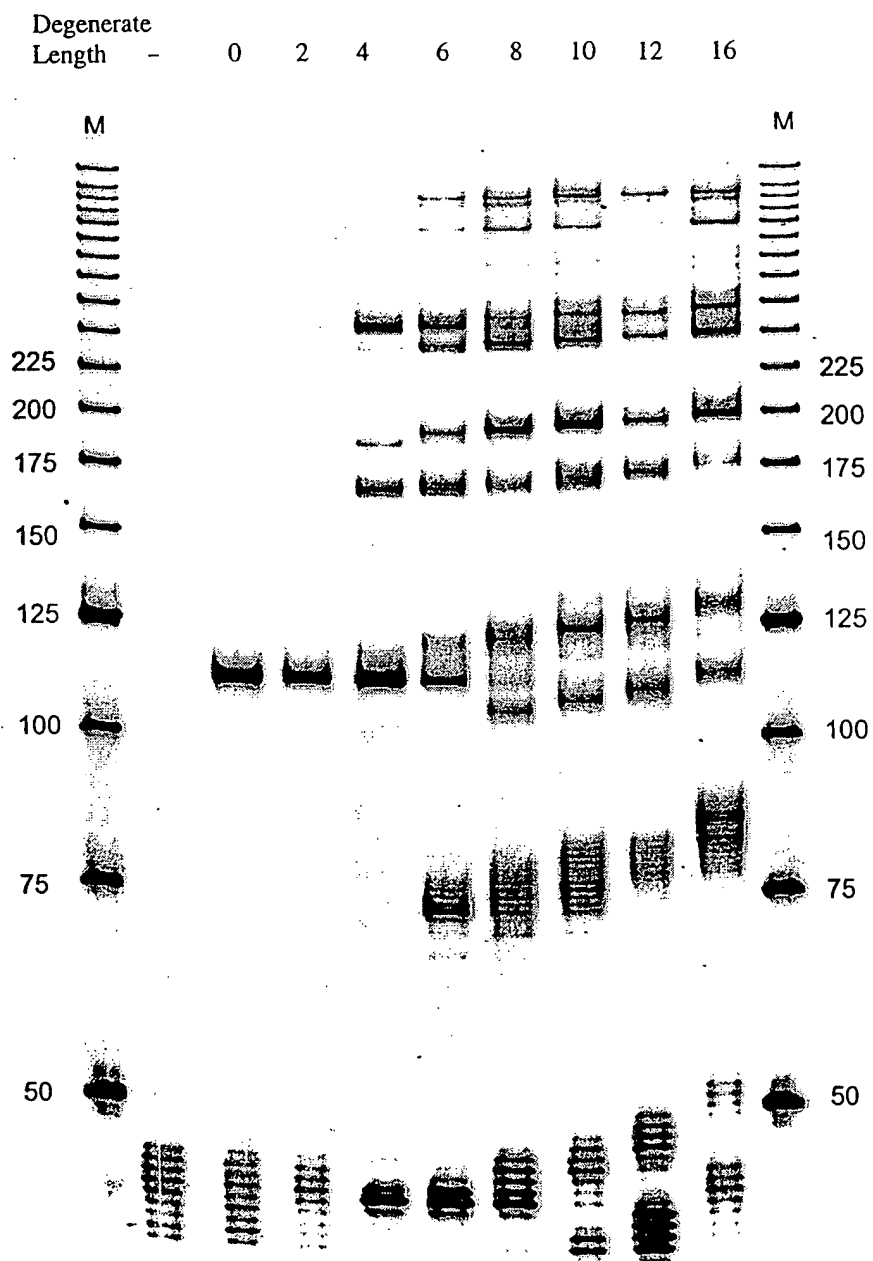


FIGURE 45A

FIGURE 46



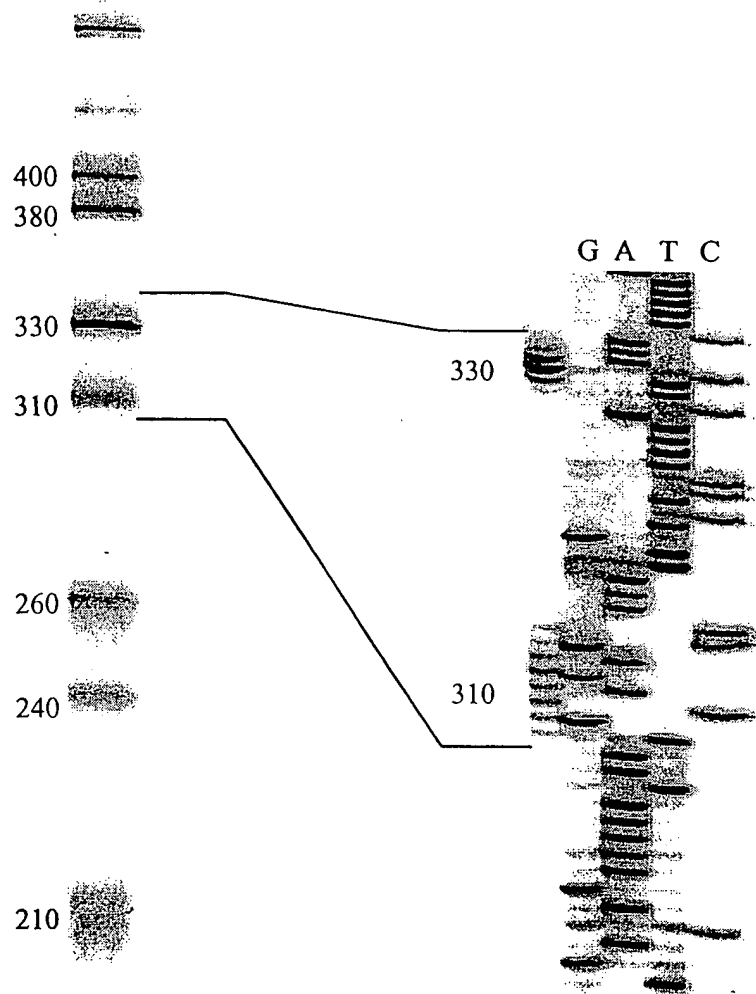


FIGURE 47

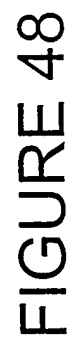


FIGURE 48

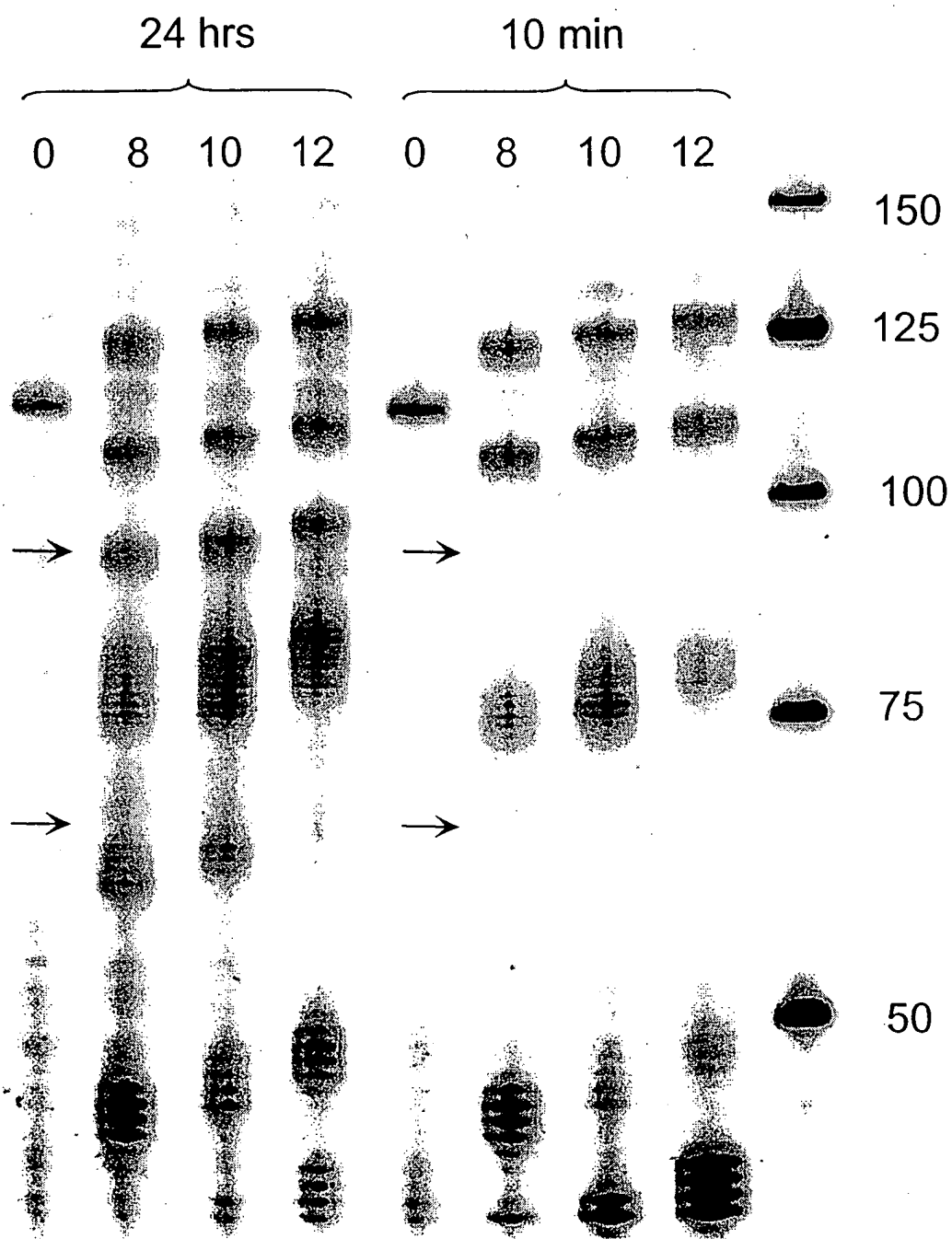


FIGURE 49

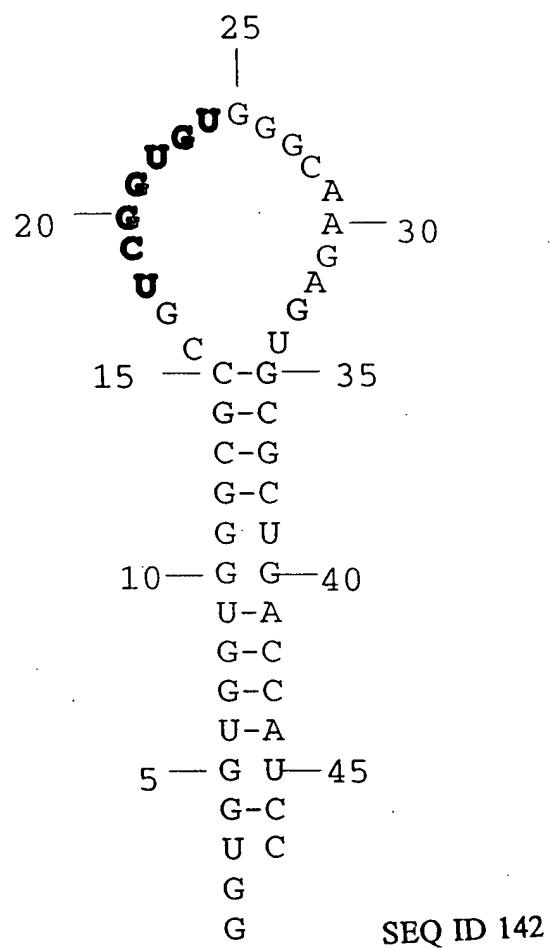


FIGURE 50A

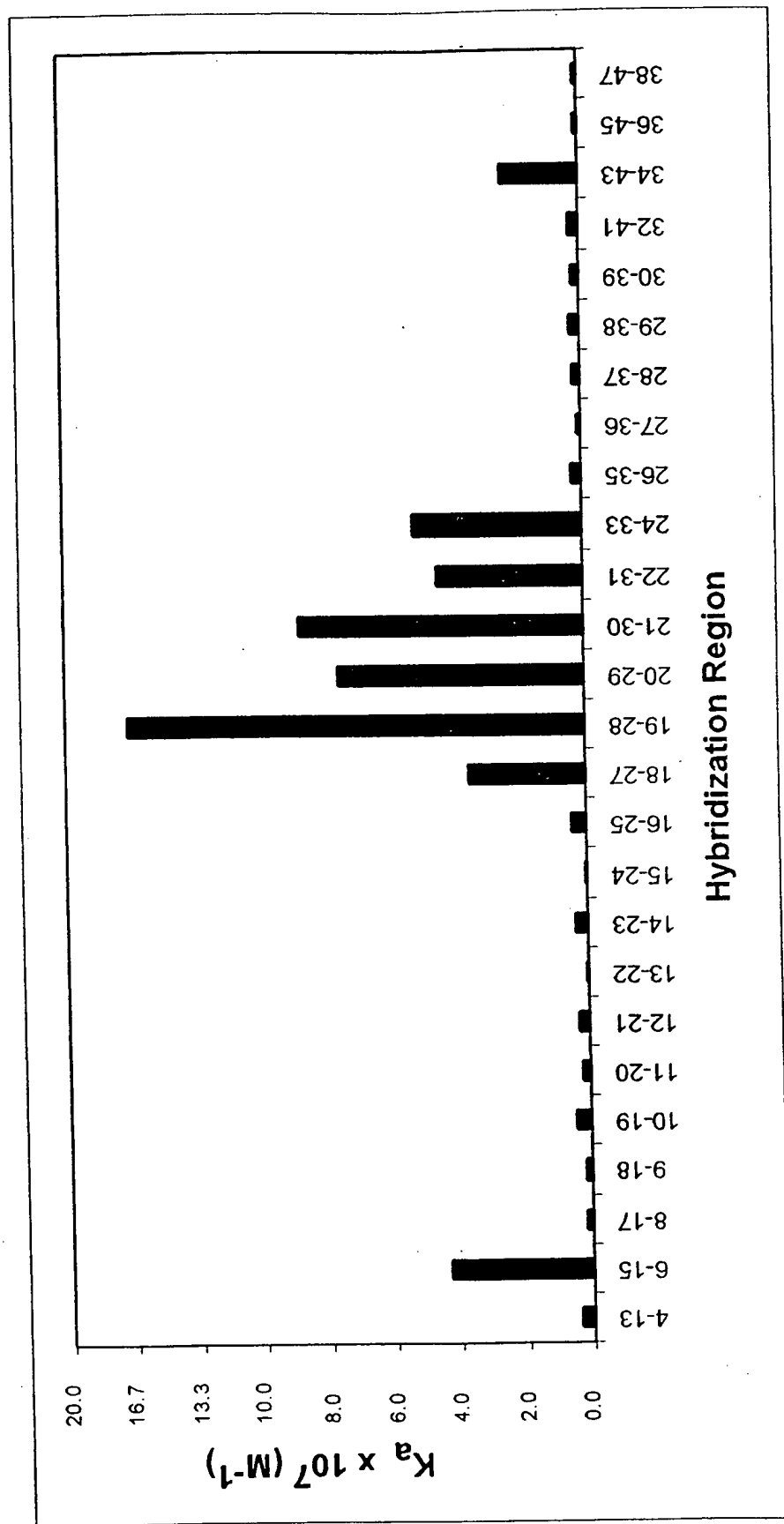


FIGURE 50B

FIGURE 51

1 ACACUUGC UU UUGACACAAC UGUGUUUACU UGCA**AAUCCCC** CAAAACAGAC

64-68 88-97

51 AGA**AUGGUGC** AUCUGUCCAG UGAGGAGA**AAG UCUGCGGUCA** CUGCCCUGUG

101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC

151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGUCCUU UGGGGACCUG

FIGURE 52A

ISIS 1571(-) ISIS 3067(+)
1 GCGCCCC AGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT

ISIS 1570(+)
41 GCA**ACCTCAG** CCTCGCTATG GCTCCCAGCA GCCCCCGGCC
81 CGCGCT**GCCC** **G**CACTCCTGG TCCTGCTCGG GGCTCTGTTC
121 CCAGGACCTG GCAATGCCCA GACATCTGTG **TCCCCCTCAA**
161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACAT**G**
201 **CAGCACCTCC** TGTGACC**AGC** **CCAAGTTGTT** GGGCATAG**AG**
241 **ACCCCGTTGC** CTAAAAAGGA GTTGCTCCTG CCTGGGAACA
281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934(-)
321 CCAACCAATG TGCTATT**CAA** ACTGCCCTGA TGGGCAGTCA
361 ACAGCTAAAA **CCTTCCTCAC** CG**TGTACTGG** ACTCCAGAAC
401 GGGTGGA**ACT** **GGCACCCCTC** **CCCTCTTGGC** AGCCAGTGGG
441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGG**CA**
481 **CCCCGGGCCA** ACCTCACCGT GGTGCTGCTC CGTGGGGAGA

FIGURE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA
as 610
561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA
601 GCCAATTTCT **CGTGCCGCAC** TGAAGTGGAC CTGCGGCCCC
641 AAGGG**CTGGA** GCTGTTTGAG AAC**ACCTCGG** **CCCC**CTACCA
681 GCTCCAGACC TTTGTCCT**TGC** **CAGCGACTCC** **CCC**ACA**ACTT**
721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG
761 TGGTCTGTTC CCT**TGGACGGG** CTGTTCCCAG TCT**CGG**AGGC
801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC
841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT
881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT
921 GACGTGTGCA GTAATACTGG GGA**ACCAGAG** **CCAGG**AGACA
961 CTGCAGACAG **TGACCATCTA** CAGCTTTCCG **GCG**CCCAACG
1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

FIGURE 52C

1041 GACAGTGAAG TGT**GAGGCC** ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA **ACGGGCGCAG**

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 **ATACACAAGA** ACCAGACCCG GGAGCTTCGT GTCCTGTAT**G**

1241 **GCCCCCGACT** GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGGCCAGAA AATT**CCCAGC** **AGACTCCAAT** GTGCCAGGCT

1321 TGGGGGAACC CATTGCCCGA GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTT**TCCC** ACTGCCCATC **GGGGAATCAG** TGACTGTCAC

1401 TCGAGATCTT **GAGGGCACCT** ACCTCTGTCG GGCCAGGAGC

1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC **ATAATGGGCA** CT**GCAGGCCT** **CAGCACGTAC**

FIGURE 52D

1561 CTCT**ATAACC** **GCCAGCGGAA** GATCAAGAAA TACAGACTAC

as 1630 as 1630h(+++)

1601 **AACAGGCCCA** **AAAAGGGACC** **CCCATG****AAAC** **CGAACACACA**

ISIS 1938 (+)

1641 **AGCCAC****GCCT** **CCCTGAACCT** **ATCCCGGGAC** **AGG**GCCTCTT

1681 **CCTCGGCCTT** CCCATATTGG TGGCAGTGGT **GCCACACTGA**

1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCT**ACCGG**

1761 **CCCTGGGACG** CCGGAGGACA GGGCATTGTC CTCAGTCAGA

1801 **TACAACAGCA** **TTTGGGGCCA** TGGTACCTGC **ACACCTAAAA**

1841 CACT**AGGCCA** **CGCATCTGAT** CTGTAGTCAC ATGACTAAGC

1881 CAAGAGGA**AG** **GAGCAAGACT** CAAGACATGA TTGATGGATG

ISIS 1939 (+)

1921 TTAAAGTCTA GCCTGAT**GAG** **AGGGGAAGTG** GTGGGGGAGA

1961 CATAGCCCCA CCAT**GAGGAC** ATACA**ACTGG** GAAATACTGA

2001 AACTTGCTGC CTATTGGGTA TGCT**GAGGCC** CACAGACTTA

2041 CAGAAG**AAGT** **GGCCCTCCAT** AGACATGTGT AGCATCAAAA

FIGURE 52E

ISIS 2302 (+)

2081 CACAAAGGCC CACACTTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGTCTA CTGACCCCAA CCCTTGATGA TATGTATTTA

ISIS 1572

2161 TTCATTTGTT ATTTTACCAG CTATTTATTG AGTGTCTTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT AACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CAAATGGGGC TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTTC TATCGGCACA AAAGCACTAT

2401 ATGGACTGGT AATGGTTCAC AGGTTCAGAG ATTACCCAGT

2441 GAGGCCTTAT TCCTCCCTTC CCCCCAAAAC TGACACCTTT

2481 GTTAGCCACC TCCCCACCCA CATACATTTT TGCCAGTGTT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC

2561 AGGGAATATG CCAAAGCTAT GCCTTGTCCT CTTGTCCTGT

FIGURE 52F

2601 TTGCATTTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

FIGURE 53A

1 CACAUUGUUC UGAUCAUCUG AAGAU CAGCU AUUAGAAGAG
 41 AAAGAU CAGU UAAGUCCUUU GGACCUGAUC AGCUUGAUAC site 80
 81 AAGAACUACU GAUUUCAACU UCUUUGGCUU AAUUCUCUCG site 120
 121 GAAACGAUGA AAUAUACAAG UUAUAUCUUG GCUUUUCAGC
 161 UCUGCAUCGU UUUGGGUUCU CUUGGCUGUU ACUGCCAGGA
 201 CCCAU AUGUA CAAGAAGCAG AAAACCUUAA GAAAU AUUUU site 210
 241 AAUGCAGGUC AUUCAGAUGU AGCGGAUAAU GGAACUCUUU site 240 site 260
 281 UCUUAGGCAU UUUGAAGAAU UGGAAAGAGG AGAGUGACAG
 321 AAAAAUAAUG CAGAGCCAAA UUGUCUCCUU UUACUUCAAA site 330
 361 CUUUUUAAAA ACUUUAAAGA UGACCAGAGC AUCCAAAAGA site 380 site 400
 401 GUGUGGAGAC CAUCAAGGAA GACAUGAAUG UCAAGUUUUU
 441 CAAUAGCAAC AAAAAGAAAC GAGAUGACUU CGAAAAGCUG

FIGURE 53B

481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG
 521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC site 560
 561 AGCAGCUAAA ACAGGGAAGC GAAAAAGGAG UCAGAUGCUG site 570
 601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC
 641 UACAAUUAUU GAAUUUUAAA UCUAAAUCUA UUUAUUAUA
 681 UUUAACAUA UUUAUAUGGG GAAUAUAUUU UUAGACUCAU
 721 CAAUCAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG
 761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUAU UUAUAAUCC
 801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA
 841 CUAUUAGGC AAGGCUAUGU GAUUACAAGG CUUUAUCUCA site 850 site 860 site 880
 881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG site 890 site 910
 921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUAU
 961 AAGUGAAGUG AUACUAUCCA GUUACUA

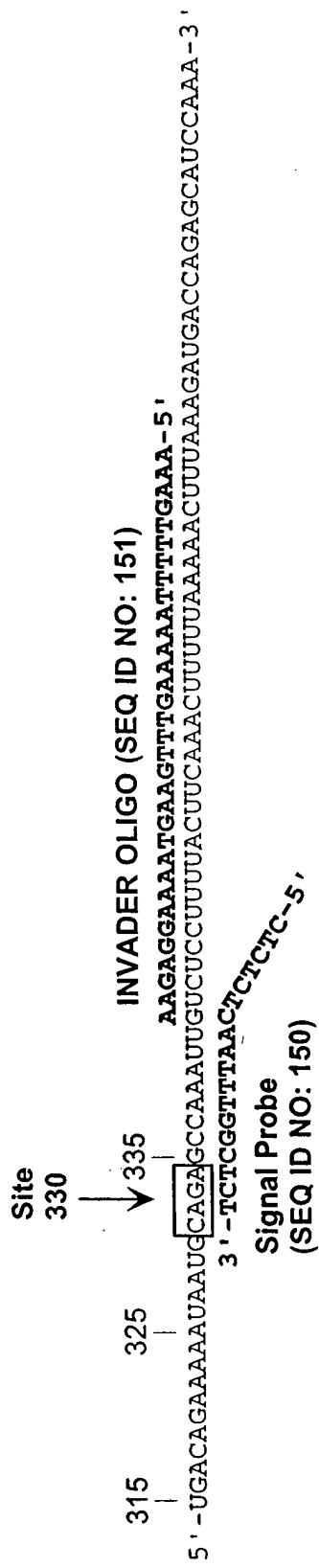


FIGURE 54A

FIGURE 54B

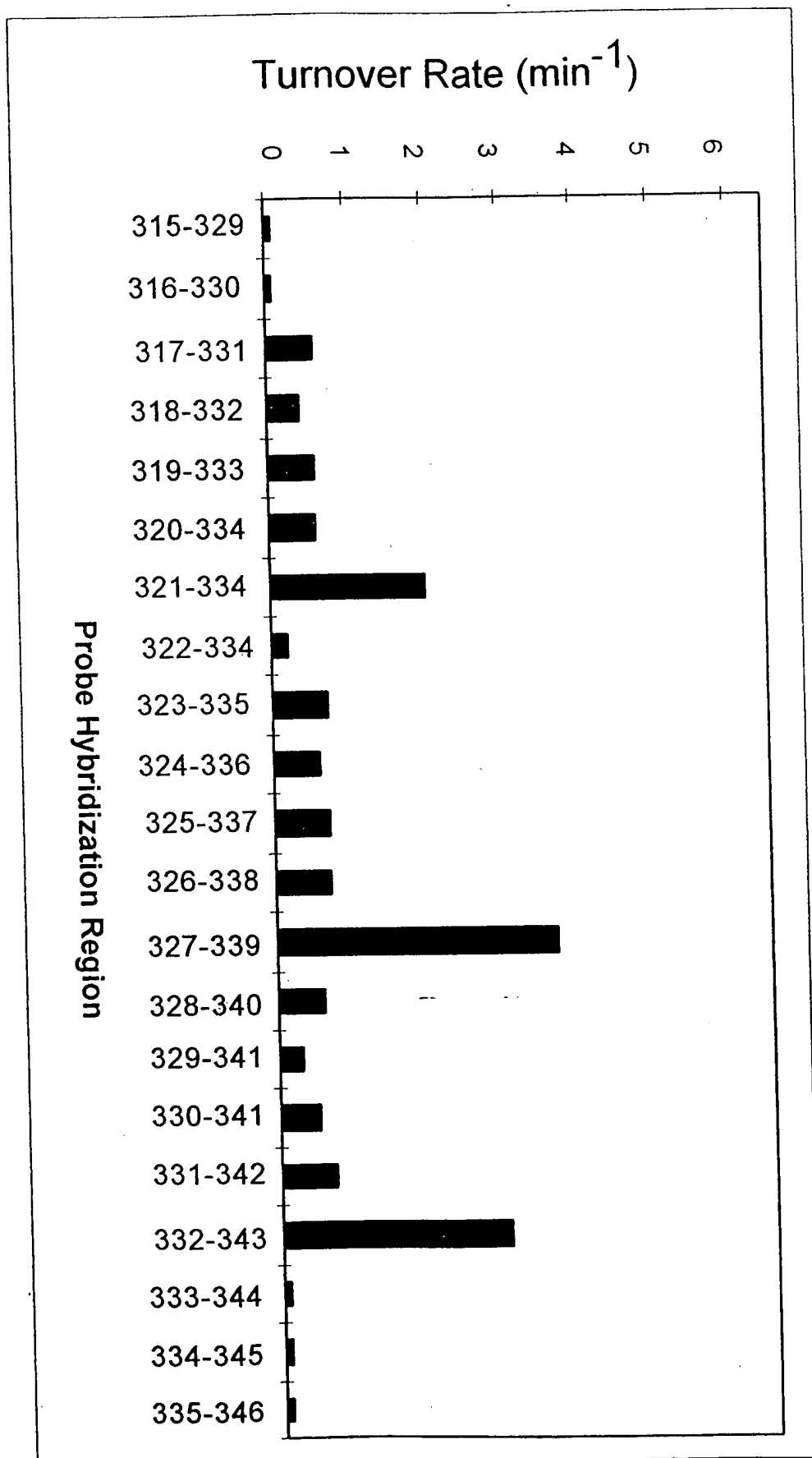


FIGURE 55A

SEQ ID NO:158

Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

Primer 3

810 UCAGUAUUAA GCGGGGGAGA AUUAGAUCGA UGGGAAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUUAAA ACAUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUAGAA

960 GGCUGUAGAC AAUACUGGG ACAGCUACAA CCAUCCCUUC AGACAGGAUC

Primer 4

1010 AGAAGAACUU AGAUCAUUAU AUAAUACAGU AGCAACCCUC UAUUGUGUGC

1060 AUCAAAGGAU AGAGAUAAAA GACAC**CAAGG** AAGCUUUAGA CAAGAUAG**AG**

FIGURE 55B

1110 **GAAGAGCAAA** ACAAAAGUAA GAAAAAAGCA CAGCAAGCAG CAGCUGACAC

1160 **AGGACACAGC** AAUCAGGUCA GCCAAAUAU CCCUAUAGUG CAGAACAUCC

Primer 5

1210 **AGGGGC**AAU GGUACAUCAG GCCAUAUCAC CUAGAACUUU AAAUGCAUGG

1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGUU

1310 UUCAGCAUUA UCAGA**AGGAG** **Cc**ACCCCAACA AGAUUUAAAC ACCAUGC~~UAA~~

1360 ACACAGUGGG GGGACAUC**A** **GC**AGCCAUGC AAAUGUUAAA AGAGACCAUC

Primer 6

1410 **AAUGAGGAAG** CUGCAGAAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC

1460 UAUUGC**ACCA** GGCCAGAUGA GAGA**ACCAAG** **GG**GAAGUGAC AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCCAGUAG GAGAAAUUUA UAAAAGAUGG AUAAUCCUGG GAUUAUUAA

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAU AGACAAGGAC

1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA

1710 **GCCGAGCAAG** CUUC**ACAGGA** GGUAAAAAU **UGGA**UGACAG AAACCUUGUU

FIGURE 55C

1760 GGUCCAAAAU GCGAACCCAG AUUGUAAGAC UAUUUUAAAA GCAUUGGGAC

Primer 8

1810 **CAGC**GGCUAC ACUAGAAGAA AUGAUGACAG CAUGUC**AGGG** AGU**AGG**AGGA

1860 CCCGGCCAUA AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

1910 UUCAGCUACC AUAUAUGAUGC **AGAGAG**GCAA UUUUAGGAAC CAAAGAAAGA

1960 UUGUUAAGUG UUUCAAUUGU GGCAAAGA**AG** **GGCACACAGC** CAGAAAUUGC

2010 AGGGCCCCUA GGAAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

2060 AAUGAAAGAU UGUACUGAGA G

FIGURE 56

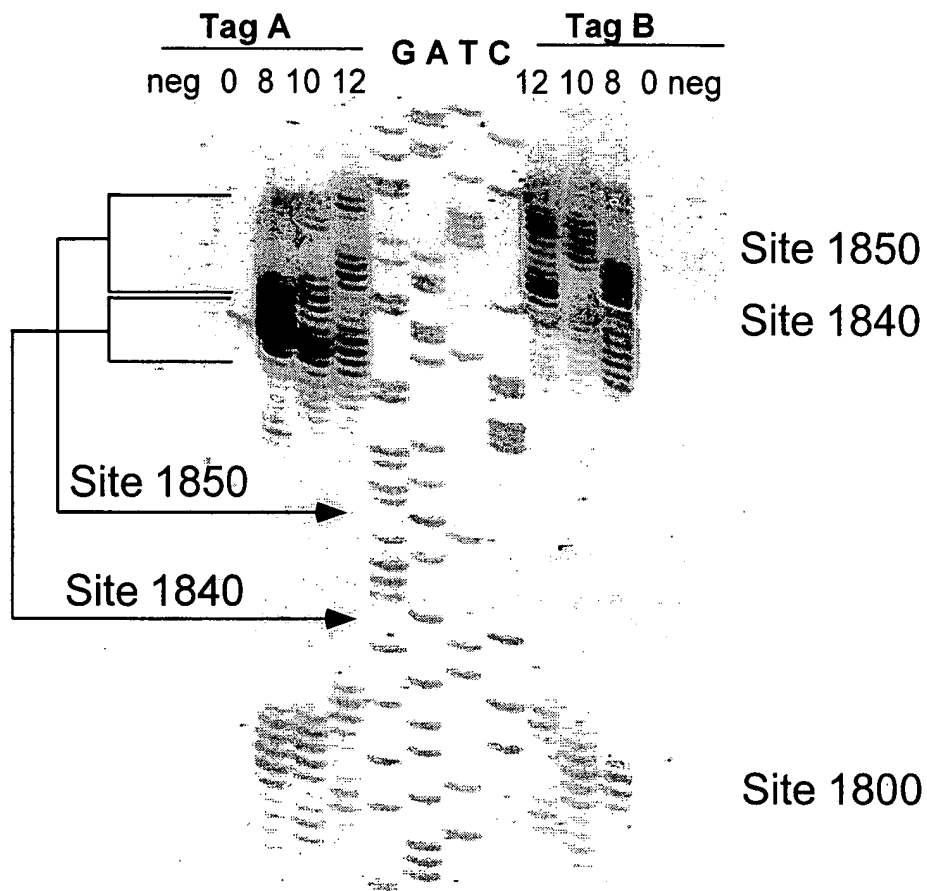


FIGURE 57

(SEQ ID NO:188)	CGTATTCCGGTCTCAAAACCGACTTGCT-5'	13
(SEQ ID NO:187)	AGGTATTCCGGTCTCAAAACCGACT	12
(SEQ ID NO:186)	ACGGTATTCCGGTCTCAAAACCGAC	10=11
(SEQ ID NO:185)	CCCGGTATTCCGGTCTCAAAACCGA	9
(SEQ ID NO:184)	CGCCGGTATTCCGGTCTCAAAACCG	8
(SEQ ID NO:183)	CGGCCGGTATTCCGGTCTCAAAAC	7
(SEQ ID NO:182)	AGGCCGGTATTCCGGTCTCAAAAC	6
(SEQ ID NO:181)	ATGGCCGGTATTCCGGTCTCAAAA	5
(SEQ ID NO:180)	ACTGGCCGGTATTCCGGTCTCAAA	4
(SEQ ID NO:179)	ACCTGGCCGGTATTCCGGTCTCAA	3
(SEQ ID NO:178)	ATCCTGGCCGGTATTCCGGTCTCA	2
(SEQ ID NO:177)	ACTCCTGGCCGGTATTCCGGTCTC	1
5'-CAUGCAGGAGUAGGACCCGGCCAUAGGCAAGUUUGGCUGAAGCAAUGAG-3'	(SEQ ID NO:158)	
1 CAGTCCCTCATC	(SEQ ID NO:164)	
2 AGTCCCTCATCC	(SEQ ID NO:165)	
3 GTCCCTCATCCT	(SEQ ID NO:166)	
4 TCCCTCATCCTC	(SEQ ID NO:167)	
5 CCCTCATCCTCC	(SEQ ID NO:168)	
6 CCTCATCCTCCT	(SEQ ID NO:169)	
7 CTCATCCTCCTG	(SEQ ID NO:170)	
8 TCATCCTCCTGG	(SEQ ID NO:171)	
9 CATCCTCCTGGG	(SEQ ID NO:172)	
10 ATCCTCCTGGGC	(SEQ ID NO:173)	
11 TCCTCCTGGGC	(SEQ ID NO:174)	
12 CCTCCTGGGCC	(SEQ ID NO:175)	
13 CTCCTGGGCCGAAA-FL-5'	(SEQ ID NO:176)	

FIGURE 58

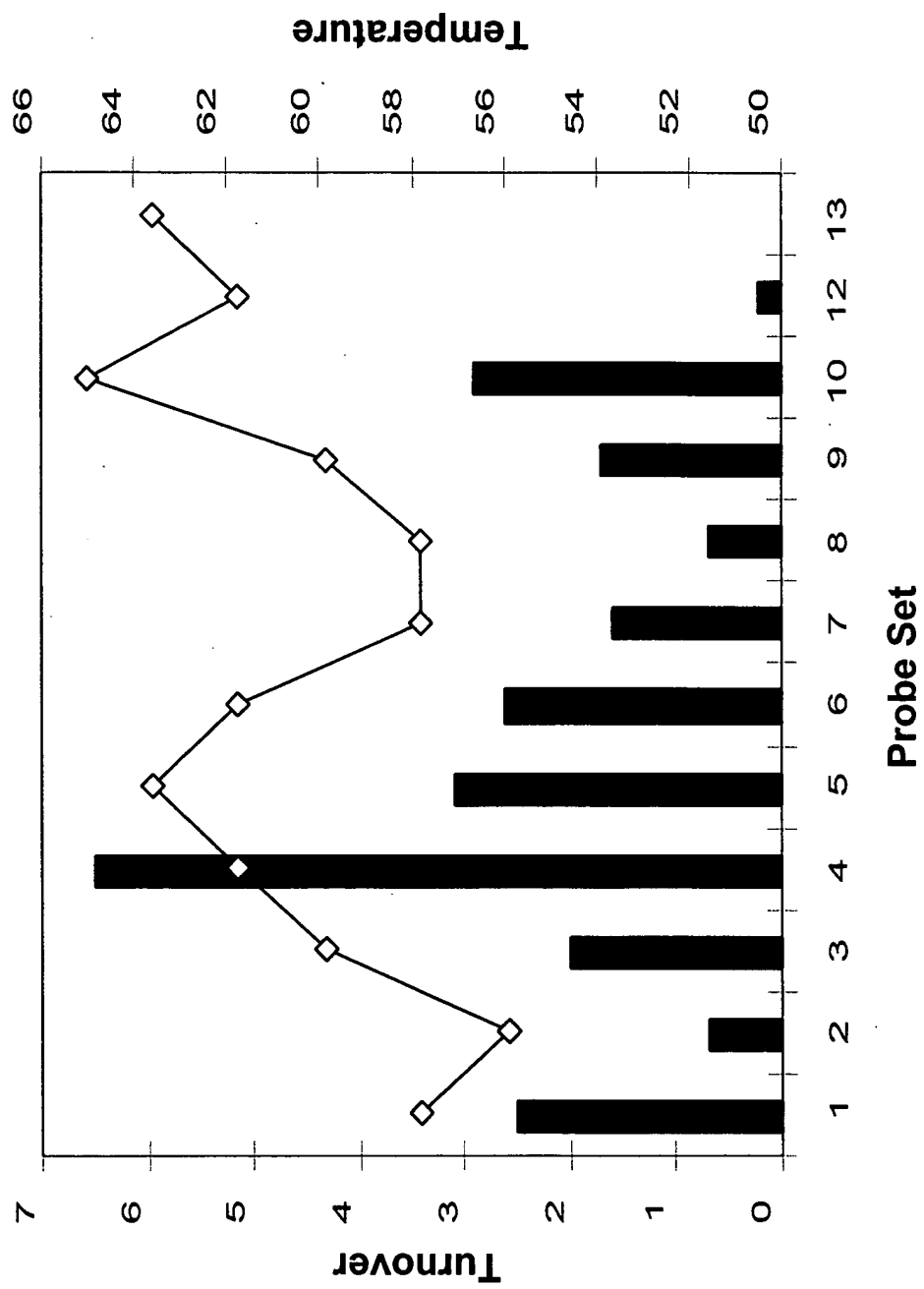


FIGURE 59

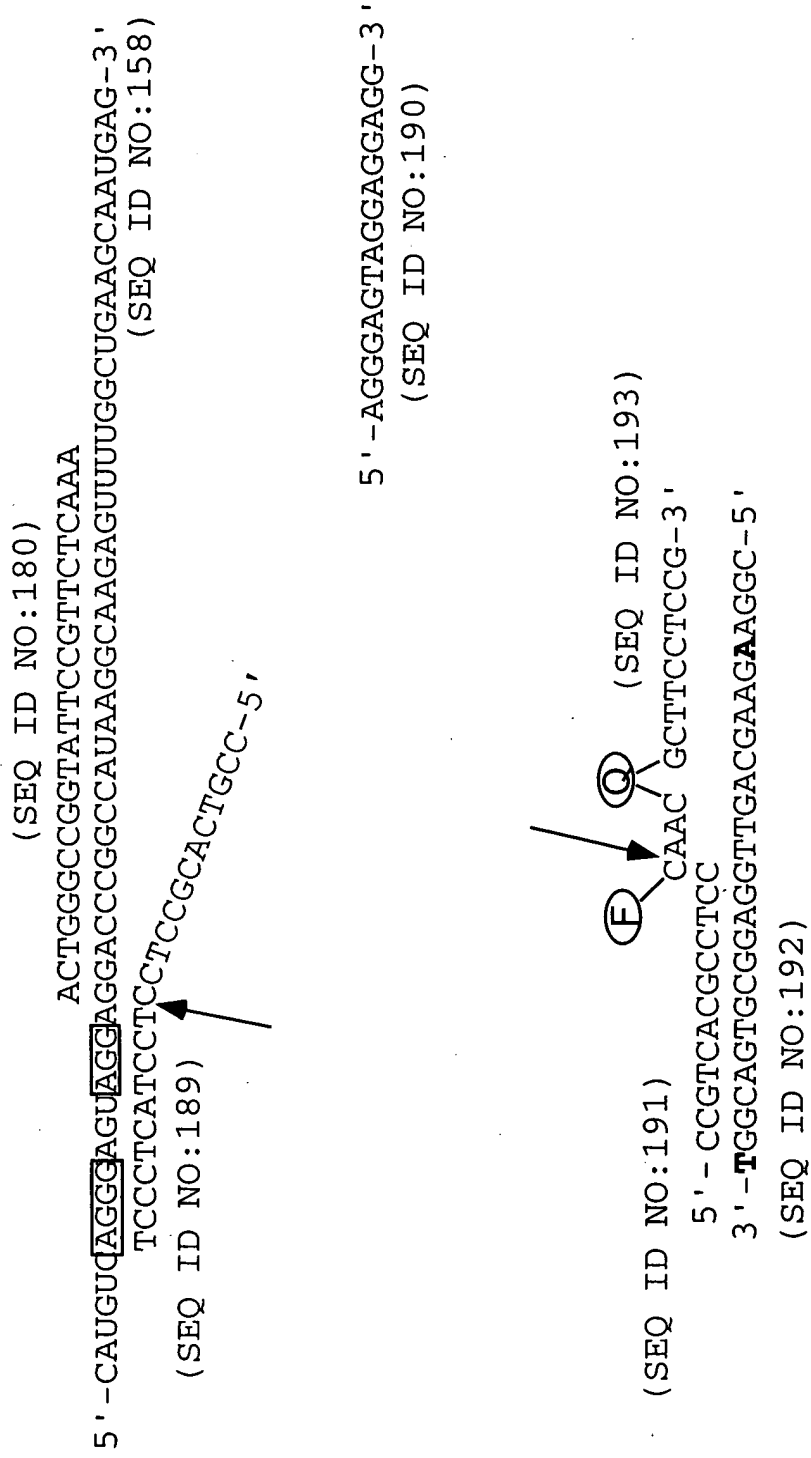


FIGURE 60

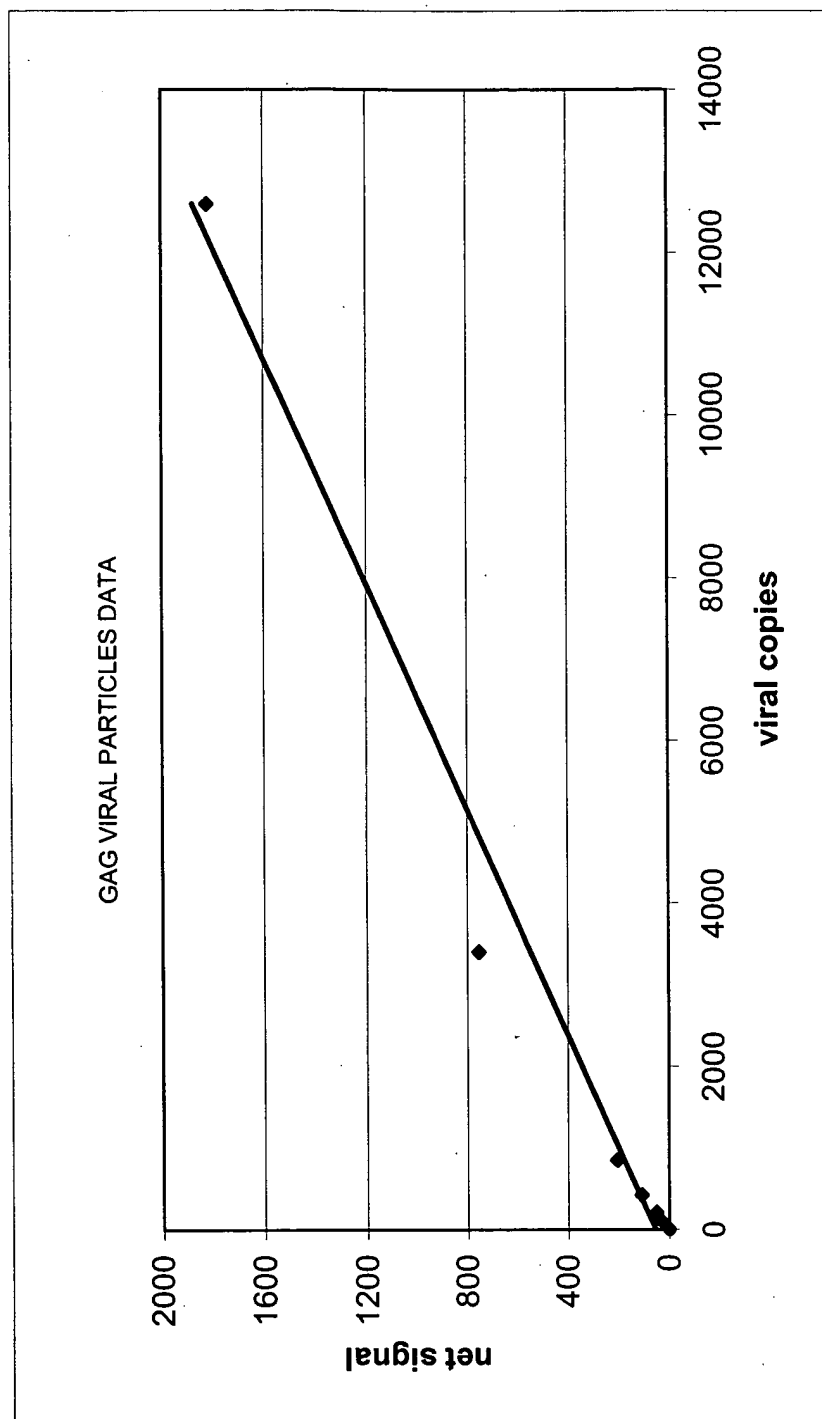


FIGURE 61A

SEQ ID NO:159

primer 1
3300 AGCUGGACUG UCAAUGACAU ACAGAA**GUUA** **GUGGGG**AAAU UG**AAUUGGGC**

3350 AAGUCAGAUU **UACCCAGGGA** UUA**AAAGUAAG** GCAAUUAUGU AAACUCCUUA

3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUAACAGA AGAAGCAGAG

3450 CUAGAA**CUGG** CAGAAAACAG AGAGAUUCUA AAAGAACCAG UACAUGGAGU

primer 2
3500 GUAUUAUGAC **CCAUCAAAAG** ACUUAUAGC AGAAAU**ACAG** **AAGCAGGGGC**

3550 **AAGGCCAAUG** GACAUAUCAA AUUUAU**CAAG** AGCCAUUUAA AAAUCUGAAA

3600 ACAGGAAAAU AUGCAAGAAU **GAGGGG**UGCC CACACUAAUG AUGUAAAACA

3650 AUUAACAG**GAG** **GCAGUG**CAAA AAUAACCAC AGAAAGCAUA GUAAUAUGGG

primer 3
3700 GAAAGACUCC UAAAUUUAAA **CUG**CCCAUAC AAAAGGAAAC AUGGGAAACA

3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU

3800 UAAUACCCCU CCCUAGUGA AAUUA**UGGUA** CCAGUUAGAG AAAGAACCCA

3850 UAGU**AGGAGC** AGAAACCUUC UAUGUAGAUG **GGGCAGCUAA** **CAGGGAGACU**

primer 4
3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU **AGAGGAAGAC** AAAAAGUUGU

FIGURE 61B

3950 CACCCUAACU GACACAACAA AUCAGAAGAC UGAGUUACAA GCAAUUUAUC
4000 UAGCUUUGCA GGAUU**CGGGA** UUAGAAGUAA ACAUAGUAAAC AGACUCACAA
4050 UAUGCAUUAG GAAUCAUUCA **AGCACAACCA** GAUCAAAGUG AAUCAGAGUU
primer 5
4100 AGUCAAUCAA AUAUA**GAGC** AGUUAUUAAA AAAGGAAAAG GUCUAUC**UGG**
4150 **CAUGGGUACC** AGCACACAAA GGA**AUUGGAG** GAAUGAACA AGUAGAUAAA
4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGA**UAA**
4250 **GGCCCAAGAU** GAACAUGAGA AAUAUCACAG UAAU**UGGAGA** GCAAUGGCUA
primer 6
4300 GUGAUUUUAA CCUGCCACCU GUAGUAGCAA AAGAAUAG**U** **AGCCAGCUGU**
4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG
4400 UCCAGGAAUA UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUAUCC
4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUUAU UAG**AAGCAGA** AGUUUUUCCA
primer 7
4500 GC**AGAAACAG** **GGCAGGAAAC** AGCAUUAUUU CUUUUAAAAU **UAGCAGGAAG**
4550 **AUGGCCAGUA** AAAACAAUAC AUAC**UGACAA** **UGGCAGCAAU** UUC**ACCGGUG**
4600 CUACGGUUAG GGCCGCCUGU UGGUGGGCGG GAAUCA**AGCA** **GGAAUUUGGA**

FIGURE 61C

4650 AUUCCCUACA AUCCCCAAAG UC**AAGG**AGUA GUAGAAUCUA UGAAUAAAGA

primer 8

4700 AUUAAAGAAA AUUAUAG**GAC** **AGG**UAAGAGA **UCAGGC**UGAA CAUCUUAAGA

4750 CAGCAGUACA AAUGGCAGUA UUCAUCCACA AUUUUAAAAG AAA**AGGGGGG**

4800 AUUGGGGGGU AC**AGUGCAGG** **GGAA**AGAAUA GUAGACAUAA UAGCAACAGA

4850 CAUACAAACU AAAGAAUUAC AAAAACAAAU UACAAAAAUU CAAAUUUUUC

primer 9

4900 GGGUUUAUUA CAG**GGAC**AGC AGAAAUCCAC UUUGGA**AAGG** ACCAGCAAAG

4950 CUCCUCUGGA AAGGUG**AAGG** GGCAGUAGUA AUACAAGAU AUAGUGACAU

5000 AAAA**GUAGUG** CCAAGAAGAA AAGCAAAGAU CAUUAGGGAU UAUGGAAAAC

5050 AGAUGGCAGG UGAUGAUUGU G

FIGURE 62

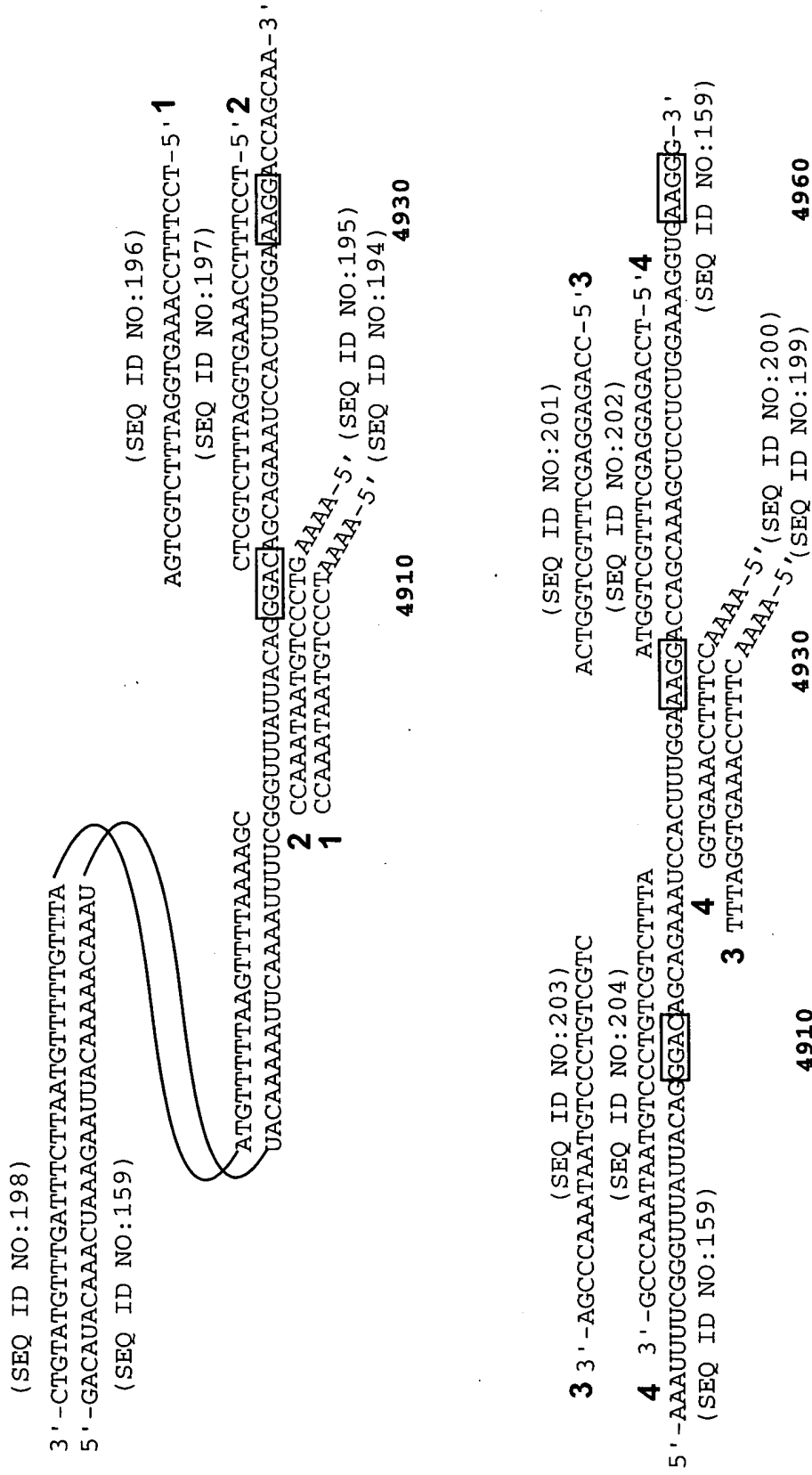


FIGURE 63

5 3' -TCCTGGTCGTTTCGAGGAGA (SEQ ID NO:213)
 6 3' -CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:214)
 5' -GAAAGGACCAGCAAAGCUCUCUGGAAAGGUGAAGGCGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUAGC-3'
 4930 6 CTTTCCACTTCCA AAA-5', (SEQ ID NO:206)
 5 CTTTCCACTTCA AAA-5', (SEQ ID NO:205)
 4960
 (SEQ ID NO:209)
 ACCCGTCATCATTTATGTTCTATTATCATCTGTATTT-5' 5
 (SEQ ID NO:210)
 ACCGTCATCATTTATGTTCTATTATCATCTGTATTTTC-5' 6
 (SEQ ID NO:159) 5000
 (SEQ ID NO:211)
 CTCATTATGTTCTATTATCATCTGTATTTTCATCACGG-5' 7
 (SEQ ID NO:212)
 ACATTATGTTCTATTATCATCTGTATTTTCATCACGG-5' 8
 5' -GAAAGGACCAGCAAAGCUCUCUGGAAAGGUGAAGGCGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUAGC-3'
 4930 8 TCCCCCGTCATA AAA-5', (SEQ ID NO:208)
 7 TTCCCCCGTCATA AAA-5', (SEQ ID NO:207)
 4960
 (SEQ ID NO:215)
 7 3' -TCGAGGAGACCTTTCCAC
 (SEQ ID NO:216)
 8 3' -TCGAGGAGACCTTTCCACT
 5' -GAAAGGACCAGCAAAGCUCUCUGGAAAGGUGAAGGCGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUAGC-3'
 4930 8 TCCCCCGTCATA AAA-5', (SEQ ID NO:208)
 7 TTCCCCCGTCATA AAA-5', (SEQ ID NO:207)
 4960

[illegible]

FIGURE 65

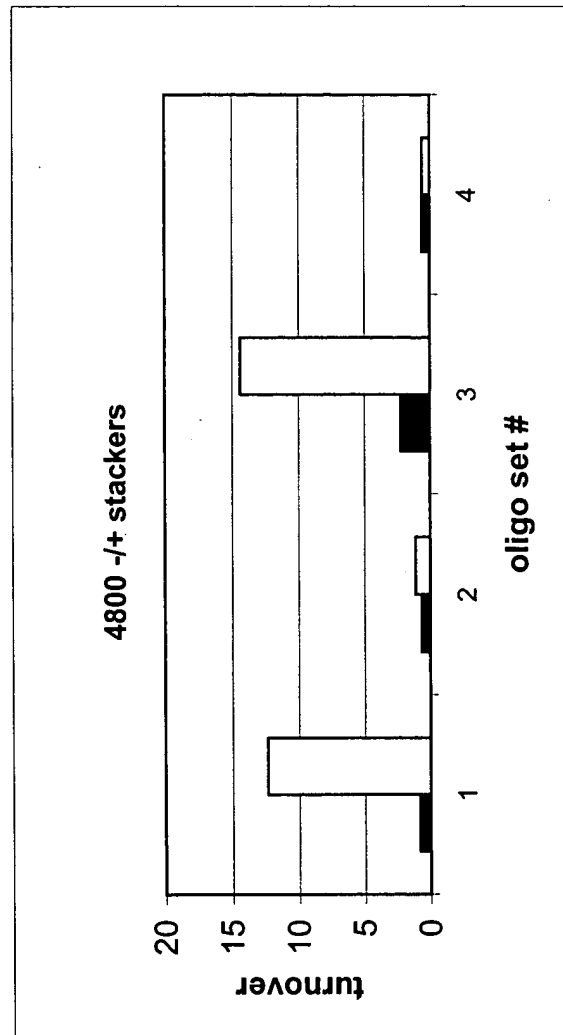


FIGURE 66

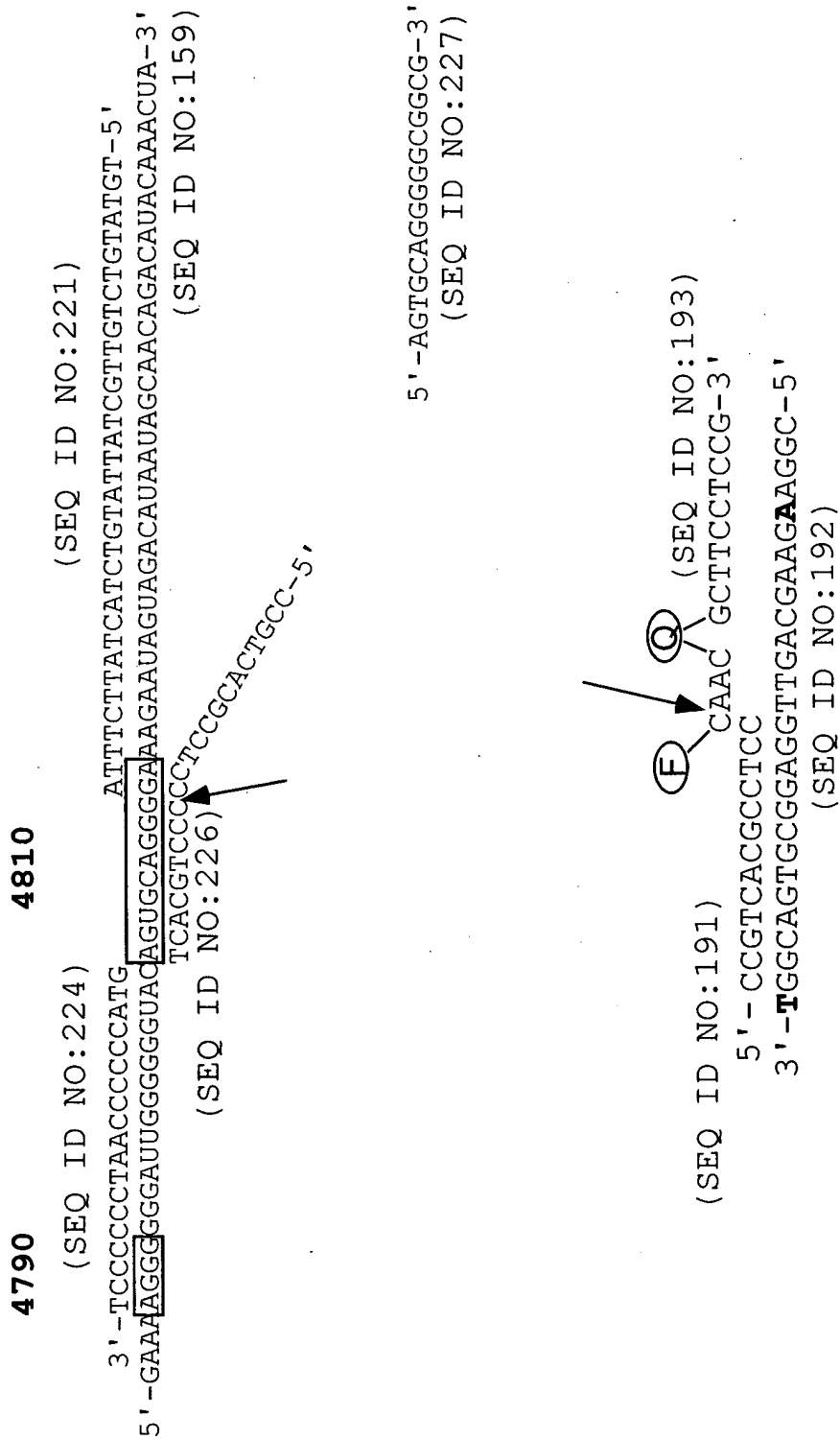


FIGURE 67

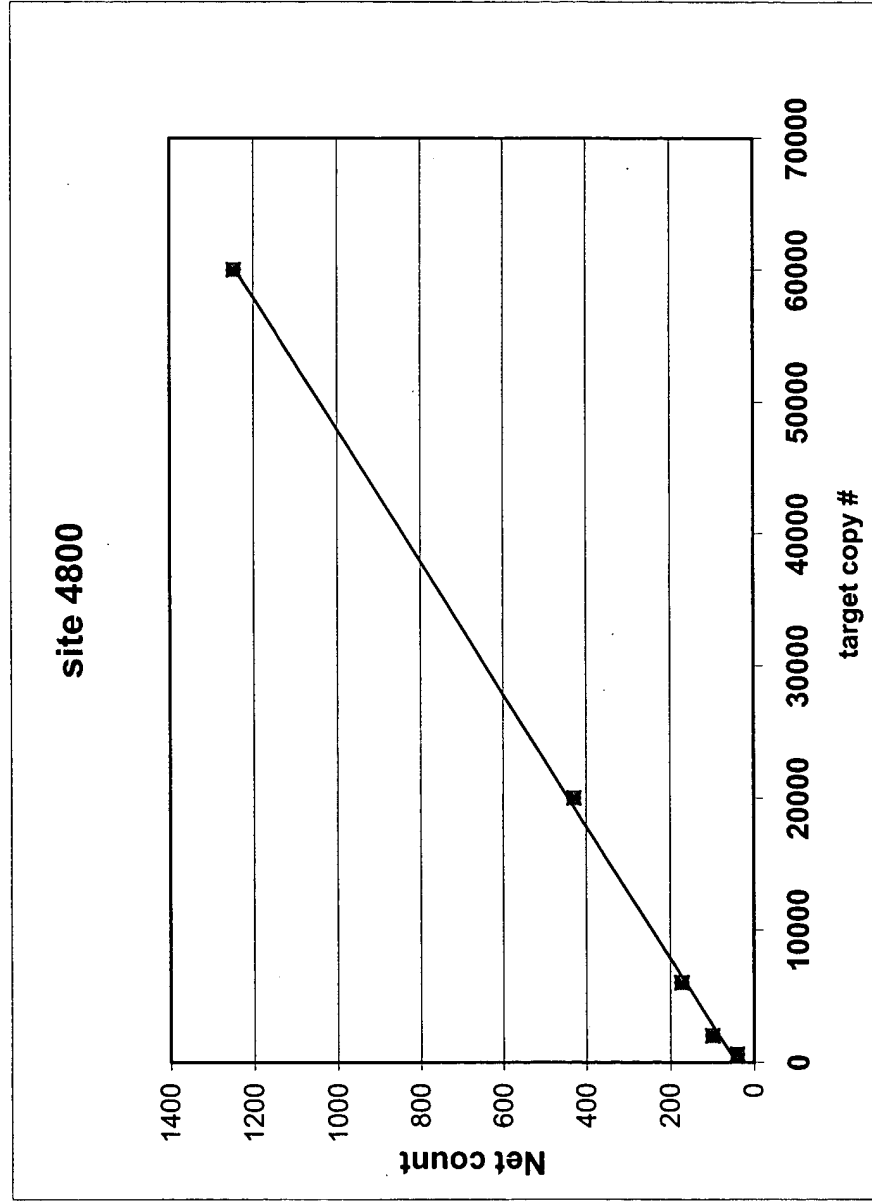


FIGURE 68

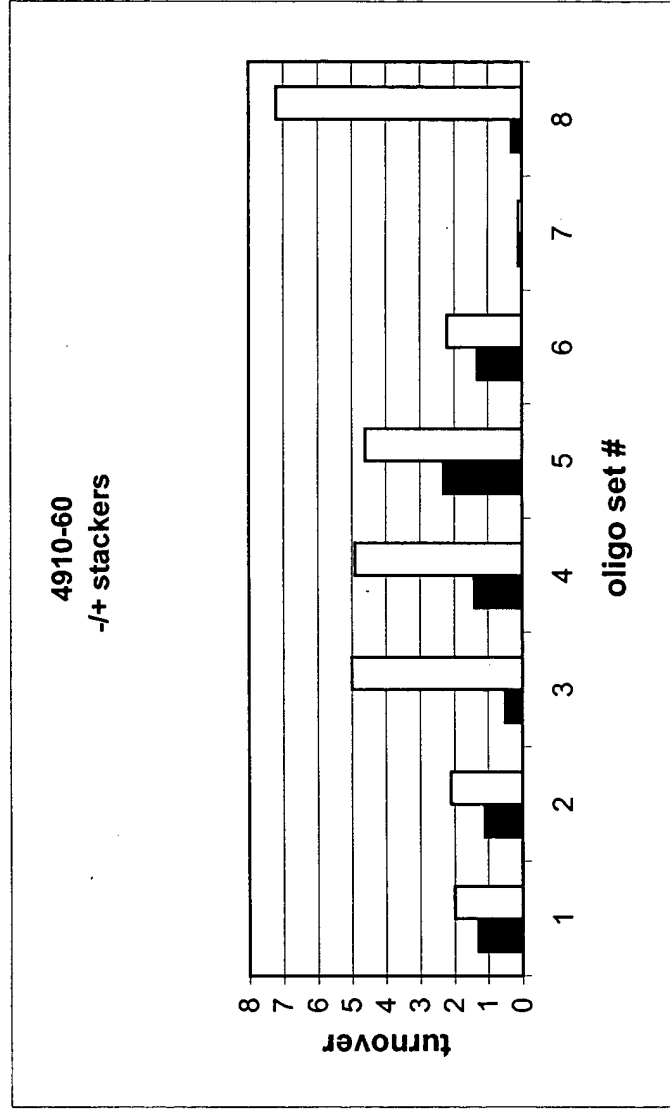


FIGURE 69

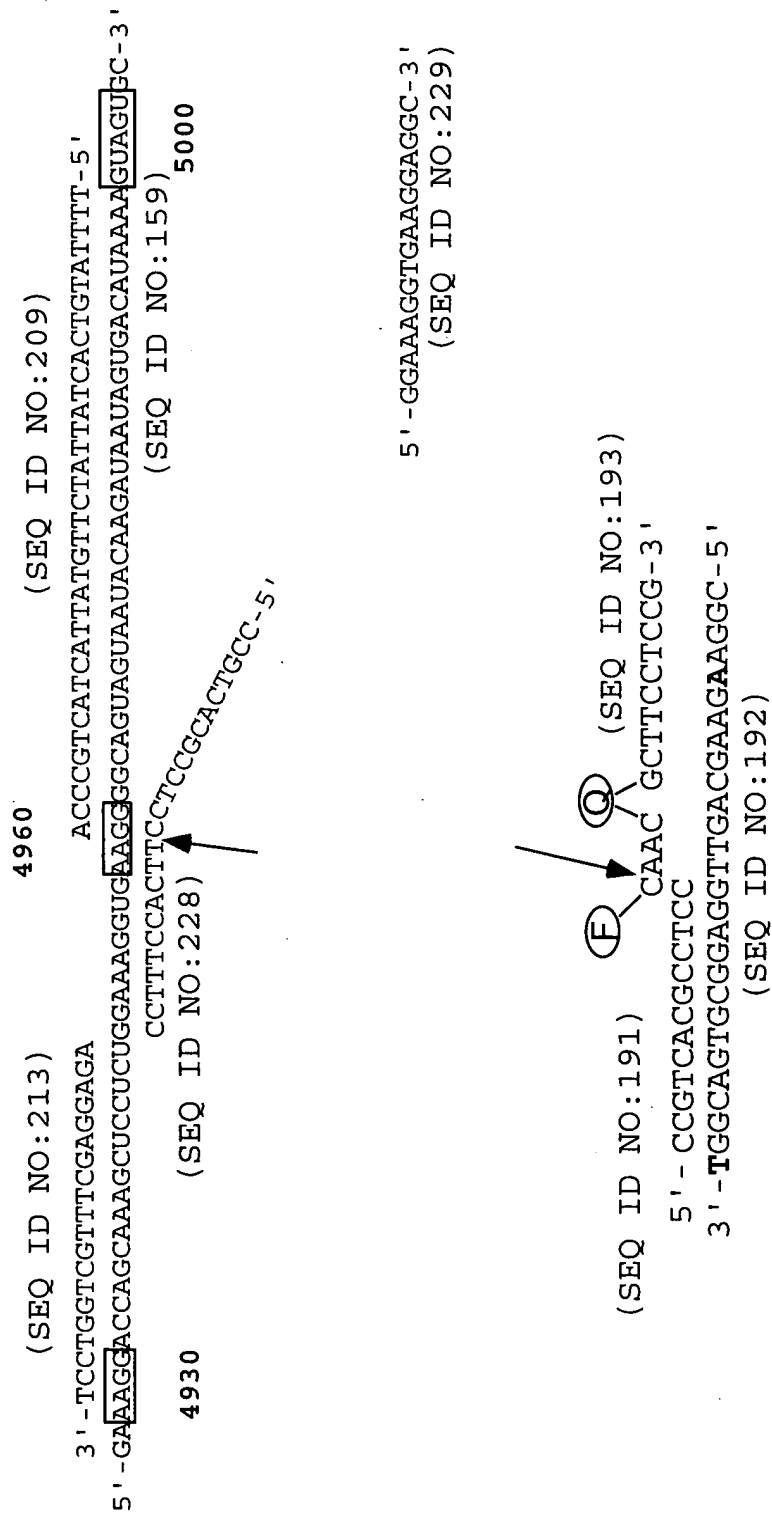


FIGURE 70

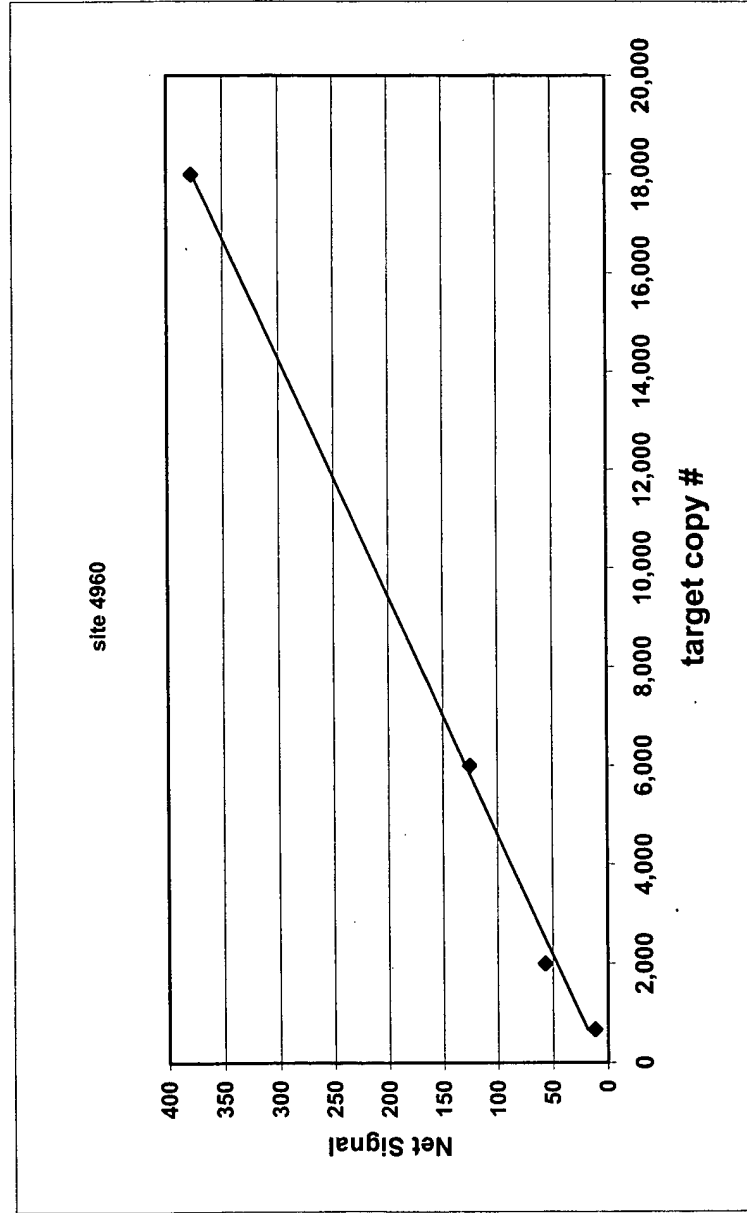


FIGURE 71

Human PSP94

383-31-1 5'-TET-CCTGCTTATCACAATGAA-3' (SEQ ID NO:230)

383-31-3 5'-TET-ACATGCACTTGCTACGAAAC-3' (SEQ ID NO:231)

SEQ ID NO:232

CCUGCUUAUCACAAUGAAUGUUCUCCUGGGCAGCGUUGUGAUCUUUGCCACCUUCGUGA
CUUUAUGCAAUGCAUCAUGCUAUUUCAUACCUAUGAGGGAGUCCAGGAGAUUCAACCA
GGAAAUGCAUGGAUCUCAAGGAAACAAACACCCAAUAAACUCGGAGUGGCAGACUGAC
AACUGUGAGACAUGCACUUGCUCGAAACAGAAAUUUCAUGUUGCACCCUUGUUUCUAC
ACCUGUGGGUUAUGACAAAGACACUGCCAAAGAAUCUUAAGAAGGAGGACUGCAAGU
AUAUCGUGGUGGAGAAGAAGGACCCAAAAAGACCUGUUCUGUCAGUGAAUGGAUAAUC
UAAUGUGCUUCUAGUAGGCACAGGGCUCCCAGGCCAGGCCUCAUUCUCCUCUGGCCUCUA
AUAGUCAAUUGAUUGUGUAGCCAUGCCUAUCAGUAAAAAGAUUUUUG

FIGURE 72

Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)

520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAAUGCAGAUUUUCGUGAAAACCCUUA^{CGG}GGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAAUGUA^{AAGGC}CAAGAUCCAGGAUAAGGAAGGAAU
UCCUCCUGACAGCAGAGACUGAUCUUUGCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUAUUCAAAAGGAGUCUACUCUUCAUCUUGUGUUGAGACUU^{CGUGGUG}G
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAA^{GCU}GGCUGUCCUGAAAUAUUUAUAAGGUGGAUGAGAAUGGC AAAAUUAGUC
GCCUUCGUCGAGAGUGCCCUUCUGAUGAAUGUGGUGCUGGGGUGUUUAUGGCAAGUCACU
UUGACAGACAUUAUUGUGGCAAAUGUUGUCUGA

FIGURE 73

HCV-1a 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUCCCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUAAACCCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCGCAAGACUGCUAGCCG
AGUAGUGUUGGUGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

FIGURE 74

HCV-1b 5'-UTR:

898-28-02 5'-TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUCCCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUCAACCCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCCCGAGACUGCUAGCCG
AGUAGUGUUGGUGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

FIGURE 75

HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGGCCCCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAUUGCCGGGAAGACUGGGUCCUUUC
UUGGAUAAACCCACUCUAUGCCCGGCCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGA
GUAGCGUUGGGUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC
GGGAGGUCUCGUAGACCGU[GCACCAUGAG]

FIGURE 76

HCV 3a 5'-UTR:

898-28-03 5'-TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUCUGUCUUCACGCGGAAAGCGC
CUAGCCAUGGCGUUAGUACGAGUGUGUGCAGCCUCCAGGCCCCCCCCUC^{CCG}GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUCGCUGGGGUGACCGGGUCCUUC
UUGGAA^{CAACCC}GCUCAAUACCCAGAAAUUUGGGCGUG^{CCCC}CGCGAGAUAC^{UAGCCG}
AGUAGUGU^{UGG}GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU^{GCACCAUGAG}

FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5'-ACAAGGGAAGAGAGATGAGGAACCAG-3'	(SEQ ID NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ ID NO:247)
937-03-01	5'-TET- aagggaagagagatgag-3'	(SEQ ID NO:248)
937-03-02	5'-TET-aggagtttgcaagaaac-3'	(SEQ ID NO:249)
937-03-03	5'-TET-ggtgctgtcctgg-3'	(SEQ ID NO:250)
937-03-04	5'-TET-cagttttggatctttgatg-3'	(SEQ ID NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ ID NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ ID NO:253)
937-03-07	5'-TET-caatactgcagatggag-3'	(SEQ ID NO:254)
937-03-08	5'-TET-aagccaggtattgca-3'	(SEQ ID NO:255)
937-03-09	5'-TET-ctattgtttctgcacaga-3'	(SEQ ID NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ ID NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ ID NO:258)

FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAAUCAUAUCCAGGA
GUUUGCAAGAAACAGGUGCUUAAACACUAAUUCACCUCCUGAACCAAGAAAUAUGGGCUGU
GACCGGAAACUGUGGGCUCaucGUGGGGCUGUCAUUGGUGCUGUCCUGGCUGUGUUUGG
AGGUAAUUCUAAUGCCAGUUGGAGACCUGCUUUAUCCAGAAGACAAUUAAGCAAGUUG
UCCUCGAAGAAGGUACA AUUGCUUUUAAAAUUGGGUUA AAAACAGGCACAGAAGUUUAC
AGACAGUUUUGGAUCUUUGAUGUGCAAAAUCCACAGGAAGUGAUGAUGAACAGCAGCAA
CAUUCAAGUUAAGCAAAGAGGUCCUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA
AUGUAACCCAGGACGCUGAGGACAACACAGUCUCUUUCCUGCAGCCCAAUGGUGCCAUUC
UUCCGAACCUUCACUAUCAGUUGGAAACAGAGGCUGACAACUUCACAGUUCUCAAUCUGGC
UGUGGCAGCUGCAUCCC AUUAUCUAUCAAAAUCAAUUUGUCAAUGAUCCUCAAUUCAC
UUAUUAACAAGUCAAAAUCUUCUAUGUCCAAGUCAGAACUUUGAGAGAACUGUUAUGG
GGCUAUAGGGAUCCAUUUUUGAGUUUGGUUCCGUACCCUGUUACUACUACAGUUGGUCUG
UUUUAUCCUUAACAACAUAACUGCAGAUGGAGUUUAUAAAGUUUUCAAUGGAAAAGAUAA
CAUAAGUAAAGUUGCCAUAAUCGACACAUUAAGGUAAAAGGAAUCUGUCCUAUUGGG
AAAGUCACUGCGACAUGAUUAAUGGUACAGAUCCAGCCUCAUUUCCACCUUUUGUUGAG
AAAAGCCAGGUUAUUGCAGUUCUUUUCUUCUGAUAUUUGCAGGUCAAUCUAUGCUGUAUU
UGAAUCCGACGUUAAUCUGAAAGGAAUCCUGUGUAUAGAUUCGUUCUCCAUCCAAGG
CCUUUGCCUCUCCAGUUGAAAACCCAAGACAACUAUUGUUUCUGCACAGAAAAAUUAUC
UCAAAAAAUUGUACAUCAUAUGGUGUGCUAGACAUCAGCAAUGCAAAGAAGGGAGACC
UGUGUACAUAUUCACUUCUCAUUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA
UGGAUUAACCCAAAUGAAGAAGAACAUAGGACAUAUUGGAUAUUAACCUAUAAUCUG
GAUUCACUUUAACA AUUUGCAAACGGCUGCAGGUCAACCUAUUGGUCAAGCAUCAGAA
AAAAUUCAAGUAUUAAGAAUCUGAAGAGGAACUAUAUUGUGCCUAUUCUUUGGCUAA
UGAGACUGGGACCAUUGGUGAUGAGAAGGCAA

FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01	5'-ATGGGGTTTGTAAAGTTG-3'	(SEQ ID NO:260)
761-47-02	5'-GCTGGGTTTAGCTCTCAGCAGCCCGC-3'	(SEQ ID NO:261)
937-05-01	5'-TET- atggggtttgttaaagtt-3'	(SEQ ID NO:262)
937-05-02	5'-TET- gaagacgacgagagg-3'	(SEQ ID NO:263)
937-05-03	5'-TET- ggatgatagttcgtgtg-3'	(SEQ ID NO:264)
937-05-04	5'-TET- gctgcagcatattgta-3'	(SEQ ID NO:265)
937-05-05	5'-TET- ctgctatttgatgca-3'	(SEQ ID NO:266)
937-05-06	5'-TET- gcagaagtacatcgga-3'	(SEQ ID NO:267)
937-05-07	5'-TET- gacatgatggaggaga-3'	(SEQ ID NO:268)
937-05-08	5'-TET- agaagaaggatcggg-3'	(SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUUGUUAAGUUGUUAAGAAUAAGGC CUACUUUAAGAGAUACCAAGUGAAAUU
 UAGAAGACGACGAGAGGGUAAAACUGAUUAUUAUGCUCGGAAACGCUUGGUGAUACAAG
 AUAAAAUAAAUAC AACACACCC AAAUACAG GAUGAUAGUUCGUGUGACAAACAGAGAU
 AUCAUUGUCAGAUUG CUUAUGCCC GUUAUAGAGGGGGAUAUGAUAGUCUGCGCACGUUA
 UGCACACGAACUGCCAAAUAUGGUGUGAAGG UUGGCCU GACAAUUAUGCUGCAGCAU
 AUUGUACUGGCCUGCUGC UGGCC CGCAGGCUUCUCAAUAGGU UUGGCAUGG ACAAGAUC
 UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAUGUGGAAAGCAUUGAUGGUCAG
 CCAGGUGCCUUCACCUGCUAUU UGGAUGCAGGCC UUGCCAGAACUACCACUGGCAAUAA
 AGUUUUUGGUGC CCUGAAGGGAGC UGUGGAUGGAG GCUUGUCUAUCCCUCACAGUACCA
 AACGAUU CCCU GGUUAUGAUUCUGAAAGCAAGGAAUUUAAUGCAGAAGUACAUC GGAAG
 CACAUC AUGG GCCAGAAUGUUGCAGAUU ACAUGCGC UACUUAU UGGAAGAAGAUGAAGA
 UGCUUACAAGAAACAGUUCUCUCAAUACAUAAGA ACAGC GUAACU CCAG ACAUGAUGG
 AGGAGAUGUAUAAGAAAGCUCAUGCUGCUAUA CGA GAGAAU CCA GUCUAUGAA AAGAAG
 CCCAA GAAAGAAGUUAAAAA GAAGAGGUGGAACCGUC CCAAAUGUCC CUU GCUCAGAA
 GAAGGAUC GGUAGCUCAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG
 AGAGCUAAACCCAGC

FIGURE 79A

Mouse Scavenger Receptor Class B Type I mRNA Oligonucleotides

726-39-01	5'-GCTCAAGAATGTCCGCATAGACCCG-3'	(SEQ ID NO:271)
666-34-01	5'-CTGGTCCCTGAGTTGTTTTTGC-3'	(SEQ ID NO:272)
937-01-01	5'-TET- GCTCAAGAATGTCCG-3'	(SEQ ID NO:273)
937-01-02	5'-TET- gggatgtggaaggag-3'	(SEQ ID NO:274)
937-01-03	5'-TET- ggaccctatgtctacag-3'	(SEQ ID NO:275)
937-01-04	5'-TET- acatcttggtcctgg-3'	(SEQ ID NO:276)
937-01-05	5'-TET- tctcaacacgtacctc-3'	(SEQ ID NO:277)
937-01-06	5'-TET- cggactcagcaaga-3'	(SEQ ID NO:278)
937-01-07	5'-TET- caaggggtgtttgaagg-3'	(SEQ ID NO:279)
937-01-08	5'-TET- ctctgtttctctccca-3'	(SEQ ID NO:280)
937-01-09	5'-TET- gtgaagatgcagctg-3'	(SEQ ID NO:281)
937-01-10	5'-TET- agctggtgctgatg-3'	(SEQ ID NO:282)
937-01-11	5'-TET- caggcctactctgag-3'	(SEQ ID NO:283)
937-01-12	5'-TET- ggactctctcagcg-3'	(SEQ ID NO:284)

FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCCGCAUAGA[CCC]GAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUAUC
CCGUCCCUUUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAAC[GAG]GUCCUC
AACGGCCAGAAGCCAGUAGU[CCGG]GAGCGUGGACCCUAUGUCUAC[AGG]GAGUUCAGACA
AAAGGUCAACAUCACCUUCAUAGA[CAACGACACC]GUGUCCUUCGUGGAGAA[CCGCAGC]C
UCCAUUUCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUUGUACUGCCUAACA
UCUUGGUCCUGGGGGGCUCAUAUUG[AUGGAG]AGCAAGCCUGUGAGCCUGAAGCUGAUG
AUGACCUUGGCGCUGGUCACCAUGGGGCCAGCGUGCUUUUAUG[AACC]GCACAGUUGGUGA
GAUCCUGUGGGGCUAUGACGAUCCCUUCGUGCAUUUUCUACAACACGUACCUCACAGACA
GCUUCCCAUAAAGGGCAAUUUGGCCUGUUGUUGGGAUGAACAACUCGAAUUC[UGG]GG
UCUUCACUGUCUUC[ACGG]GCGUCCAGAAUUUC[AGCA]GGAUCCAUCUGGUGGACAAAUGG
AACGGACUCAGCAAGAUCGAUUAU[UGGCAUUCAGAGCA]GUGUAACAUGAUCAA[UGG]GAC
U[UCCGG]GCAGAUG[UGGGC]ACCCUUCA[UGACACC]CGA[AUCCUC]GCUGGAAUUCUUCAGCC
[CGGA]GGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAUU
CCCACGUAUCGCUUC[ACGGCC]CCCGAUACUCUGUUUGCCAACGGGUCCGUCUACCCACC
CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGUU
UGGUGCGCCUCUGUUUCUCUCCCAACCCACUUUUAC[AACGCCGAC]CCUGUGUUGUCAG
AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUUCUUGUUCUAGACAUCCA[U]
[CCGGU]CACUGGGAUCCCCAUGAACUGUUCUGUGAAGAU[GCA]GC[UGA]GCCUCUACAUCAA
AUCUGUCAAGGGCAUCGGGCAAACAGGGAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG
GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCACGUUCUACACGCAGCUGGU
GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGGCUUGGAGGCCUCCU
GUUGCUGGUGCCCAUCAUCUGCCAACUGCGC[AGCCAGGA]GAAUGCUUUUUGUUUUGGA
GUGGUAGUAAAAAGGGCUCCAGGAUAAGGAGGCCAUUCAGGCCUACUCUGAGUCCUGA
UGUCACCAGCUGCCAAGGGCACGGUGCUGCAAGAAGCCAAGCUAUAGGGUCCUGAAGACA
CUAUAAG[CCCC]CCAAACCUGAUAGCUUGGUCAGACCAGCCACCCAGUCCCUACACCCCG
CUUCUUGAGGACUCUCUCAGCGGACAGCCCACCAGUGCCAUGGCCUGAGCCCCCAGAUGU
CACACCUGUCCGCACGCACGGCACAUGGAUGCCCACGCAUGUGCAAAAACAACUCAGGGA
CCAG

FIGURE 80A

Rat CX3CR1 Accession No. U04808 Oligonucleotides

761-57-01	5'-taatacgactcactatagggacggaagtccaagagcatcactg-3'	(SEQ ID NO:286)
761-57-03	5'-gcaggtagctgggtccgta-3'	(SEQ ID NO:287)
781-65-01	5'-TET-ggaagtccaagagca-3'	(SEQ ID NO:288)
781-65-02	5'-TET-aatggcttctttggg-3'	(SEQ ID NO:289)
781-65-03	5'-TET-ggcgtcgccc-3'	(SEQ ID NO:290)
781-65-04	5'-TET-tacttccgcatcgtc-3'	(SEQ ID NO:291)
781-65-05	5'-TET-cttcttccctagttgtg-3'	(SEQ ID NO:292)
781-65-06	5'-TET-tgcctggccgt-3'	(SEQ ID NO:293)
781-65-07	5'-TET-gactctactaagaaccca-3'	(SEQ ID NO:294)
781-73-01	5'-TET-ccatcttagtggcgt-3'	(SEQ ID NO:295)
781-73-02	5'-TET-caacaagtgcctgg-3'	(SEQ ID NO:296)
781-85-01	5'-TET-aacacggcgtcac-3'	(SEQ ID NO:297)
781-85-02	5'-TET-tgattaccccgagg-3'	(SEQ ID NO:298)
781-85-03	5'-TET-acgctgttttcctg-3'	(SEQ ID NO:299)
781-85-04	5'-TET-tgagacacctgtacaa-3'	(SEQ ID NO:300)
781-85-05	5'-TET-gacggagacagtgg-3'	(SEQ ID NO:301)
781-85-06	5'-TET-caagcgaggagag-3'	(SEQ ID NO:302)

FIGURE 80B

Rat CX3CR1 Accession No. U04808 (SEQ ID NO:303)

[illegible]

FIGURE 81A

Human Interleukin-1 beta (IL-1 β) Oligonucleotides

720-82-01 5'-
gtaatttaatacgaactcactatagggaaggtgcagttttgccaaggagtgcataag-3'
(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatttatctaataaaacatcat-3'
(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3' (SEQ ID NO:306)
781-50-02 5'-TET-gagagtggaccacac-3' (SEQ ID NO:307)
781-50-03 5'-TET-gaatcagtgaagatgcc-3' (SEQ ID NO:308)
781-50-04 5'-TET-cattgtaccatgaaatatcc-3' (SEQ ID NO:309)
781-50-05 5'-TET-gaactttaatttcaggaattg-3' (SEQ ID NO:310)
781-50-06 5'-TET-ccctagtctgctagc-3' (SEQ ID NO:311)
781-50-07 5'-TET-ttcaagtgtacttattaacc-3' (SEQ ID NO:312)
781-72-01 5'-TET-aagctggccgtg-3' (SEQ ID NO:313)
781-72-02 5'-TET-tgcagttttgccaag-3' (SEQ ID NO:314)

FIGURE 81B

**Human Interleukin-1 beta (IL-1 β) (GenBank Accession #
M15330) (SEQ ID NO:315)**

GGCAGAAGUACCUGAGCUCGCCAGUGAAUGAUGGCUUAUUA CAGUGGCAAUGAGGAUG
ACUUGUUCUUUGAAGCUGAUGGC CCUAAACAGAUGAAGUGCUCUCCAGGACCUGGAC
CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAAUCU CCGACCAC CACUA CAGCAAGG
CUUCAGGCAGGCCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUU C
CCUGCC CACAGACCUUCCAGGAGAAUGA CCUG AGCACCUUCUUCUCCUUCUUCUUGAA
GAAGAACCUAUCUUCUUCG ACACAUGG GAU AACGA GGCUUAUGUG CACGA UGCACCUGU
ACGAUC ACUGAACUGCACGCUC CGGACUCACAGCAAAAAGCUUGGUGAUGUCUGGUC
CAUAUGAACUGAAAGCU CUCC ACCUC CAG GGGACAGGAUAUGGAGCAACAAGUGGUGUUC
UCCAUGUCCUUGUACAAGGAGAAGAAAGUAAUGACAAAUACCUGUGGCCUUGGGCCUC
AAGGAAAAGAAUCUGUAC CUGUCCUGCG UGUUGAAAGAUGAUAAAGCCCACUCUACAGCU
GGAGAGUGUAGAUC CAAAAUUA C C C C C A A A A A G A A G A A G G A A A A G C G A U U G U C U U C A A
CAAGAUAGAAAUCAAU AACAAAGCU GGAAUUGAG UCUG CCCAGU U C C C C A A C U G G U A C A
UCAGCACCC UCUC AAGCAGAAAA CAUGC CCGUCU UCCUGGGAGGGACCAAAG GCGG C CAG
GAUAUAACUGACUUC ACCA UGCAAUUUGUGUCU UCCUAAAGAGAGCUGUACCCAGAGAG
UCCUGUGCUGAAUGUGGACUCAAUCC CUAGGGCU GGCAGAAAGGGAACAGAAAGGUUUU
UGAGUACGGCUAUAGCCUGGACUUUCCUGUUGUCUACACCAAUGCCCAACUGCCUGCCUU
AGGGUAGUGCUAAGAGGAUCUCCUGUCCA UCAGCCA GGACAGUCAGCUCUCUCCUUU CA
GGGCCAAUCC CCAGC CCUUUUGUU GAGCCAGGCCUCUCUCAC CUCUCCUACUCACUU AA
AGCCCGCC UGACAGA AACACGG CCACA UUGGUUCUAAGAAACCUCUGUCAUUCGCU
CCCACA UUCUGAU GAGCAACCGCU UCCCUAUUUU AUUU AUUU AUUU UGUUUUGUUUUUA
UUCAUUGGUCUAAUUUAUU CAAAGGGGGC AAGAAGUAGCAGUGUCUGUAAAAGAGCCUA
GUUUUUA AUAGCUAUGGAAUCAAUUCAAUUGGA CUG GUGUGCUCUCUUUAAAUCAAGU
CCUUUAA UUAAGAC UGAAAUAU AUAAGCU CAGAUUAUUU AAAUG GGAUAUUUAUAA A
UGAGCAAAUAUCAUACUGUUA

FIGURE 82A

Human Interferon gamma Oligonucleotides

448-59-01	5'-TET-GCATCGTTTTGGGTTCTCTT	(SEQ ID NO:316)
448-59-02	5'-TET-ACTTTAAAGATGACCAGAGC	(SEQ ID NO:317)
448-79-01	CACATTGTTCTGATCATCTG	(SEQ ID NO:318)
448-79-02	CGGTAAGTGAATGTC	(SEQ ID NO:319)
448-79-03	TAGTAAGTATATCAC	(SEQ ID NO:320)
448-79-04	GACATTCAAGTCAGTTACCG	(SEQ ID NO:321)
498-20-01	AATTTAATACGACTCACTATACACATTGTTCTGATCATCTG	(SEQ ID NO:322)
498-20-02	AATTTAATACGACTCACTATACGGTAAGTGAATGTC	(SEQ ID NO:323)
498-20-03	5'-TET-CACATTGTTCTGATCATCTG	(SEQ ID NO:324)
498-20-04	5'-TET-CGGTAAGTGAATGTC	(SEQ ID NO:325)
498-40-01	5'- AGTAATTTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA	(SEQ ID NO:326)
498-40-02	5'- AGTAATTTACGACTCACTATAGGGACGGTAAGTGAATGTCCAAC	(SEQ ID NO:327)
498-84-01	5'-TET-CATTCAGATGTAGCG	(SEQ ID NO:328)
498-84-02	5'-TET-GACTCATCAATCAAA	(SEQ ID NO:329)
498-84-03	5'-TET-GATTACAAGGCTTTA	(SEQ ID NO:330)

FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCaucUGAAGAUCAGCUAUUAGAAGAGAAAGAUcAGUUAAGUCCUUU
GGACCUGAUCAGCUUGAUACAAGAACUACUGAUUUCAACUUCUUUGGCUUAAUUCUCUC
GGAAACGAUGAAAUAUACAAGUUUAUcUUGGCUUUUCAGCUCUGCAUCGUUUUGGGUUC
UCUUGGCUGUACUGCCAGGACCCAUUGUACAAGAAGCAGAAAACCUUAAGAAAUAUU
UUAUGCAGGUCAUUCAGAUGUAGCGGAUAAUGGAACUCUUUUCUUAGGCAUUUUGAAG
AAUUGGAAAGAGGAGAGUGACAGAAAAUAUGAGAGCCAAAUUGUCUCCUUUUACUU
CAAACUUUUUAAAAACUUUAAAGAUGACCAGAGCAUCCAAAAGAGUGUGGAGACCAUCA
AGGAAGACAUGAAUGUCAAGUUUUCAAUAGCAACAAAAGAAACGAGAUGACUUCGAAA
AGCUGACUAAUUAUUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA
UCCAAGUGAUGGCUGAACUGUCGCCAGCAGCUAAAACAGGGAAGCGAAAAAGGAGUCAG
AUGCUGUUUCGAGGUCGAAGAGCAUCCAGUAAUGGUUGUCCUGCCUACAAUAUUUGAAU
UUUAAAUCUAAAUcUAUUUAUUAAUAUAACAUAUAUUUAUAUGGGGAUAUAUUUUUAGAC
UCAUCAAUCAAUAAGUAUUUAUAAUAGCAACUUUUGUGUAAUGAAAAUGAAUAUCUAUU
AAUAUAUGUAUAUUUAUAAUCCUAUAUCCUGUGACUGUCUCACUUAUCCUUUGUUUU
CUGACUAAUAGGCAAGGCUAUGUGAUUACAAGGCUUUAUCUCAGGGGCCAACUAGGCA
GCCAACCUAAGCAAGAUCCCAUGGGUUGUGUGUUUAUUUCACUUGAUGAUACAAUGAAC
ACUUAUAAGUGAAGUGAUACUAUCCAGUUACUA

FIGURE 83A

Pneumocystis carinii (NUCLEOTIDES 84-415 OF ACCESSION #
AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGUGAUCUGGAAUAAAUUCAGAUUGC
GACACUGUCAAAUUGC GGGGAAGCCCUAAAGAUUCAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAUAGCCCUUGGUUAUAGUAACAAUGUUGAAUAUGAAUCUUUU
GCGAGAUGAAAUGGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG
UUCAACGACUAGAUGGCAGUGGGUAUUGUAAGGAAUUGCAGUUUUCUUGCAGUGCUUAA
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGUAUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION #
X74272) (SEQ ID NO:332)

GGGAGGCAAAAGUAGGGACGCCAUGGUUUCAGAAAUGGGCCGCGGUGUUUUUGACCUGC
UAGUCGAUCUGGCCAGACGUUUCUGUGGGUGGCCAGCGGCGACAUAACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UGGGGUUAAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCGUAGAG
CAGCGAAAGGUAUGGGCUGGCUCUCUGAGUCGGCUUAAAGUACGUGCCGUCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUUCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

FIGURE 83B

Earwig R2 element (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCUCUCAGCUGCUCACUUGCUGUUCUAAGUG
AUAAUACCGUUGUUUUUUUAGUGGGUAUUCUUUUACGCUUUCGUAGGAGCGAGUCCCAC
ACUCUUGGAGCAAUCCGGGGUAGUGCCUAAACGCAUUUCUUCAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAAGGGUGUAGAUCAGGCCCGUCUGUUUCUCCCCGGA
GCUCGCUCCCUUGGCUUCCCUUAUAUAUUUUAACAUCAGAAACAGACAUUAAACAUCUA
CUGAUCCAAUUUCGCCGGCGUACGGCCACGAUCGGGAGGGUGGGAAUCUCGGGGGUCUU
CCGAUCCUAAUCCAUGAUGAUUACGACCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC
GGCGAUG